

MAR 25 2002

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Tue Jun 18 15:59:27 2001 [BLASTN 2.1.3 [Apr-1-2001], NCBI]  
/home/ruby/va/Molbio/carpenda/temp1/ss.DNA35639 (1813 bp)

MAR 27 2002

TECH CENTER 1600/2900

BLAST RESULTS A-1

Sequences producing High-scoring Segment Pairs:

		Frame	Score	Match	Pct	E-val
1	P_AAC97441 Human angiogenesis-associated protein PR	+	1813	1813	100	0.0
2	P_AAF72379 Human PRO246 cDNA.	+	1813	1813	100	0.0
3	P_AAC87040 Nucleotide sequence of human polypeptide	+	1813	1813	100	0.0
4	P_AAF60372 PRO246 coding sequence.	+	1813	1813	100	0.0
5	P_AAA30052 Human PRO246 nucleotide sequence.	+	1813	1813	100	0.0
6	P_AAX28436 EGF-like homologue PRO246 coding sequenc	+	1813	1813	100	0.0
7	P_AAX52221 Protein PRO246 cDNA clone DNA35639-1172.	+	1813	1813	100	0.0
8	AX076924 Sequence 36 from Patent WO0105836.	+	1813	1813	100	0.0
9	P_AAF93785 Human cDNA encoding a membrane or secret	+	1809	1809	100	0.0
10	AX136161 Sequence 83 from Patent EP1067182.	+	1809	1809	100	0.0
11	P_AAA23441 cDNA encoding human secreted protein vc5	+	1806	1813	100	0.0
12	AF361746 Homo sapiens endothelial cell-selective	+	1805	1811	100	0.0
13	P_AAH02949 Human shear stress-response coding seque	+	1801	1807	100	0.0
14	P_AAZ65278 Human secreted protein gene 29.	+	1785	1804	100	0.0
15	P_AAF45017 Human secreted protein related coding se	+	1731	1795	99	0.0
16	P_AAF45016 Human secreted protein related coding se	+	1731	1795	99	0.0
17	P_AAF45014 Human secreted protein related coding se	+	1731	1795	99	0.0

>1 P\_AAC97441 Human angiogenesis-associated protein PRO246 cDNA, SEQ ID NO:95.  
(1813 bp) [1 seg]

Score = 1813 (3594 bits), Expect = 0.0

Identities = 1813/1813 (100%), at 1,1-1813,1813, Strand +/+

DNA35639 1 GGAGCCGCCCTGGGTGTCAGCGCTCGGCTCCCGCGCACGCTCCGGCGTCGCGCAGCCT  
\*\*\*\*\*  
P\_AAC97441 1 GGAGCCGCCCTGGGTGTCAGCGCTCGGCTCCCGCGCACGCTCCGGCGTCGCGCAGCCT  
  
DNA35639 61 CGGCACCTGCAGGTCCGTGCGTCCCAGCGCTGGCGCCCTGACTCCGTCCGGCCAGGGA  
\*\*\*\*\*  
P\_AAC97441 61 CGGCACCTGCAGGTCCGTGCGTCCCAGCGCTGGCGCCCTGACTCCGTCCGGCCAGGGA  
  
DNA35639 121 GGGCCATGATTCCCTCCGGGCCCTGGTGACCAACTTGCTGCGGTTTTGTTCTGG  
\*\*\*\*\*  
P\_AAC97441 121 GGGCCATGATTCCCTCCGGGCCCTGGTGACCAACTTGCTGCGGTTTTGTTCTGG  
  
DNA35639 181 GGCTGAGTGCCTCGCGCCCCCTCGCGGGCCCAGCTGCAACTGCACTTGCCCCGCCAAC  
\*\*\*\*\*  
P\_AAC97441 181 GGCTGAGTGCCTCGCGCCCCCTCGCGGGCCCAGCTGCAACTGCACTTGCCCCGCCAAC  
  
DNA35639 241 GGTTGCAGGCGGTGGAGGGAGGGGAAGTGGTGCTTCCAGCGTGGTACACCTTGACCGGGG  
\*\*\*\*\*  
P\_AAC97441 241 GGTTGCAGGCGGTGGAGGGAGGGGAAGTGGTGCTTCCAGCGTGGTACACCTTGACCGGGG  
  
DNA35639 301 AGGTGTCTTCATCCCAGCCATGGGAGGTGCCCTTGTGATGTGGTTCTCAAACAGAAAG  
\*\*\*\*\*  
P\_AAC97441 301 AGGTGTCTTCATCCCAGCCATGGGAGGTGCCCTTGTGATGTGGTTCTCAAACAGAAAG  
  
DNA35639 361 AAAAGGAGGATCAGGTGTTGCTTACATCAATGGGGTCACAACAAGCAAACCTGGAGTAT  
\*\*\*\*\*  
P\_AAC97441 361 AAAAGGAGGATCAGGTGTTGCTTACATCAATGGGGTCACAACAAGCAAACCTGGAGTAT

BLAST RESULTS A-2

DNA35639	421	CCTTGGTCTACTCCATGCCCTCCCGAACCTGTCCCTGCGGCTGGAGGGCTCCAGGAGA *****
P_AAC97441	421	CCTTGGTCTACTCCATGCCCTCCCGAACCTGTCCCTGCGGCTGGAGGGCTCCAGGAGA *****
DNA35639	481	AAGACTCTGGCCCTACAGCTGCCGTGAATGTGCAAGACAAACAAGGCAAATCTAGGG *****
P_AAC97441	481	AAGACTCTGGCCCTACAGCTGCCGTGAATGTGCAAGACAAACAAGGCAAATCTAGGG *****
DNA35639	541	GCCACAGCATAAAACCTTAGAACTCAATGTACTGGTCCTCAGCTCCATCCTGCC *****
P_AAC97441	541	GCCACAGCATAAAACCTTAGAACTCAATGTACTGGTCCTCAGCTCCATCCTGCC *****
DNA35639	601	GTCTCCAGGGTGTGCCCATGTGGGGCAAACGTGACCTGAGCTGCCAGTCTCCAAGGA *****
P_AAC97441	601	GTCTCCAGGGTGTGCCCATGTGGGGCAAACGTGACCTGAGCTGCCAGTCTCCAAGGA *****
DNA35639	661	GTAAGCCGCTGTCCAATACCAGTGGGATCGGCAGCTCCATCCTCCAGACTTTCTTG *****
P_AAC97441	661	GTAAGCCGCTGTCCAATACCAGTGGGATCGGCAGCTCCATCCTCCAGACTTTCTTG *****
DNA35639	721	CACCAGCATTAGATGTCATCCGTGGTCTTAAGCCTCACCAACCTTCGTCTCCATGG *****
P_AAC97441	721	CACCAGCATTAGATGTCATCCGTGGTCTTAAGCCTCACCAACCTTCGTCTCCATGG *****
DNA35639	781	CTGGAGTCTATGTCTGCAAGGCCACAATGAGGTGGGACTGCCAATGTAATGTGACGC *****
P_AAC97441	781	CTGGAGTCTATGTCTGCAAGGCCACAATGAGGTGGGACTGCCAATGTAATGTGACGC *****
DNA35639	841	TGGAAGT GAGCACAGGCCCTGGAGCTGCAGTGGTGTGGAGCTGTTGGTACCTGG *****
P_AAC97441	841	TGGAAGT GAGCACAGGCCCTGGAGCTGCAGTGGTGTGGAGCTGTTGGTACCTGG *****
DNA35639	901	TTGGACTGGGTTGCTGGCTGGCTGGCTCTTGATACCACGCCGGGGCAAGGCCCTGG *****
P_AAC97441	901	TTGGACTGGGTTGCTGGCTGGCTGGCTCTTGATACCACGCCGGGGCAAGGCCCTGG *****
DNA35639	961	AGGAGCCAGCCAATGATATCAAGGAGGATGCCATTGCTCCCCGACCTGCCCTGGCCA *****
P_AAC97441	961	AGGAGCCAGCCAATGATATCAAGGAGGATGCCATTGCTCCCCGACCTGCCCTGGCCA *****
DNA35639	1021	AGAGCTCAGACACAATCTCCAAGAACATGGGACCCCTTCCTCTGTCACCTCCGCACGAGCCC *****
P_AAC97441	1021	AGAGCTCAGACACAATCTCCAAGAACATGGGACCCCTTCCTCTGTCACCTCCGCACGAGCCC *****
DNA35639	1081	TCCGGCCACCCATGGCCCTCCAGGCCCTGGTGCATTGACCCCCACGCCAGTCTCTCCA *****
P_AAC97441	1081	TCCGGCCACCCATGGCCCTCCAGGCCCTGGTGCATTGACCCCCACGCCAGTCTCTCCA *****
DNA35639	1141	GCCAGGCCCTGCCCTCACCAAGACTGCCACGACAGATGGGGCCACCTCAACCAATAT *****
P_AAC97441	1141	GCCAGGCCCTGCCCTCACCAAGACTGCCACGACAGATGGGGCCACCTCAACCAATAT *****
DNA35639	1201	CCCCCATCCCTGGTGGGTTCTCCTCTGGCTTGAGCCGATGGGTGCTGTGCCTGTGA *****
P_AAC97441	1201	CCCCCATCCCTGGTGGGTTCTCCTCTGGCTTGAGCCGATGGGTGCTGTGCCTGTGA *****
DNA35639	1261	TGGTGCCTGCCAGAGTCAGCTGGCTCTGGTATGATGACCCACACTCATTGGCTA *****

# BLAST RESULTS A-3

\*\*\*\*\*  
P\_AAC97441 1261 TGGTGCCTGCCAGAGTCAGCAGCTGGCTCTGGTATGACCCACCCTCATGGCTA  
DNA35639 1321 AAGGATTGGGTCTCTCCTATAAGGGCACCTCTAGCACAGAGGCCTGAGTCATG  
\*\*\*\*\*  
P\_AAC97441 1321 AAGGATTGGGTCTCTCCTATAAGGGCACCTCTAGCACAGAGGCCTGAGTCATG  
DNA35639 1381 GGAAAGAGTCACACTCCTGACCCTAGTACTCTGCCCAACCTCTTTACTGTGGGAA  
\*\*\*\*\*  
P\_AAC97441 1381 GGAAAGAGTCACACTCCTGACCCTAGTACTCTGCCCAACCTCTTTACTGTGGGAA  
DNA35639 1441 ACCATCTCAGTAAGACCTAACAGTGTCCAGGAGACAGAAGGAGAAGAGGAAGTGGATCTGGA  
\*\*\*\*\*  
P\_AAC97441 1441 ACCATCTCAGTAAGACCTAACAGTGTCCAGGAGACAGAAGGAGAAGAGGAAGTGGATCTGGA  
DNA35639 1501 ATTGGGAGGAGCCTCCACCCACCCCTGACTCCTCTTATGAAGCCAGTGCTGAAATTAG  
\*\*\*\*\*  
P\_AAC97441 1501 ATTGGGAGGAGCCTCCACCCACCCCTGACTCCTCTTATGAAGCCAGTGCTGAAATTAG  
DNA35639 1561 CTACTCACCAAGAGTGAGGGGCAGAGACTTCCAGTCACTGAGTCTCCAGGCCCTTGA  
\*\*\*\*\*  
P\_AAC97441 1561 CTACTCACCAAGAGTGAGGGGCAGAGACTTCCAGTCACTGAGTCTCCAGGCCCTTGA  
DNA35639 1621 TCTGTACCCCACCCCTATCTAACACCACCCCTGGCTCCACTCCAGCTCCCTGTATTGAT  
\*\*\*\*\*  
P\_AAC97441 1621 TCTGTACCCCACCCCTATCTAACACCACCCCTGGCTCCACTCCAGCTCCCTGTATTGAT  
DNA35639 1681 ATAACCTGTCAGGCTGGTTAGGTTACTGGGGCAGAGGATAGGAAATCTCTTAT  
\*\*\*\*\*  
P\_AAC97441 1681 ATAACCTGTCAGGCTGGTTAGGTTACTGGGGCAGAGGATAGGAAATCTCTTAT  
DNA35639 1741 TAAAACTAACATGAAATATGTGTTTTCTATTGCAAATTAAAGATACTAAATG  
\*\*\*\*\*  
P\_AAC97441 1741 TAAAACTAACATGAAATATGTGTTTTCTATTGCAAATTAAAGATACTAAATG  
DNA35639 1801 TTTGTATGAAAAA  
\*\*\*\*\*  
P\_AAC97441 1801 TTTGTATGAAAAA

>2 P\_AAF72379 Human PRO246 cDNA. (1813 bp) [1 seg]

Score = 1813 (3594 bits), Expect = 0.0

Identities = 1813/1813 (100%), at 1,1-1813,1813, Strand +/+

DNA35639 1 GGAGCCGCCCTGGGTGTCAGCGGCTCGGCTCCCGCGCACGCTCCGGCCGTGCGCAGCCT  
\*\*\*\*\*  
P\_AAF72379 1 GGAGCCGCCCTGGGTGTCAGCGGCTCGGCTCCCGCGCACGCTCCGGCCGTGCGCAGCCT  
DNA35639 61 CGGCACCTGCAGGTCCGTGCGTCCCGCGCTGGCAGGCCCTGACTCCGTCCGGCCAGGGA  
\*\*\*\*\*  
P\_AAF72379 61 CGGCACCTGCAGGTCCGTGCGTCCCGCGCTGGCAGGCCCTGACTCCGTCCGGCCAGGGA  
DNA35639 121 GGGCCATGATTCCCTCCGGGGCCCTGGTGACCAACTTGCTGCGGTTTTGTTCCCTGG  
\*\*\*\*\*  
P\_AAF72379 121 GGGCCATGATTCCCTCCGGGGCCCTGGTGACCAACTTGCTGCGGTTTTGTTCCCTGG  
DNA35639 181 GGCTGAGTGCCTCGGCCCGCCCTCGCGGGCCAGCTGCAACTGCACTTGCCCCGCCAAC  
\*\*\*\*\*

Blast results A-4

P_AAF72379	181	GGCTGAGTGCCCTCGGCCCGCCCTCGCGGGCCCAGCTGCAACTGCAC	TGCCCCGCCAAC
DNA35639	241	GGTTGCAGGCGGTGGAGGGAGGGAAAGTGGTGCTTCCAGCGTGGTACAC	CTTGCACGGG *****
P_AAF72379	241	GGTTGCAGGCGGTGGAGGGAGGGAAAGTGGTGCTTCCAGCGTGGTACAC	CTTGCACGGG *****
DNA35639	301	AGGTGTCTTCATCCCAGCCATGGGAGGTGCCCTTGTGATGTGGTTCTC	AAACAGAAAG *****
P_AAF72379	301	AGGTGTCTTCATCCCAGCCATGGGAGGTGCCCTTGTGATGTGGTTCTC	AAACAGAAAG *****
DNA35639	361	AAAAGGAGGATCAGGTGTTGCTTACATCAATGGGGTACAACAAGCAAAC	CTGGAGTAT *****
P_AAF72379	361	AAAAGGAGGATCAGGTGTTGCTTACATCAATGGGGTACAACAAGCAAAC	CTGGAGTAT *****
DNA35639	421	CCTTGGTCTACTCCATGCCCTCCCGAACCTGTCCTGCGGCTGGAGGG	TCTCCAGGAGA *****
P_AAF72379	421	CCTTGGTCTACTCCATGCCCTCCCGAACCTGTCCTGCGGCTGGAGGG	TCTCCAGGAGA *****
DNA35639	481	AAGACTCTGGCCCTACAGCTGCTCCGTGAATGTGCAAGACAAACAAG	GCAAATCTAGGG *****
P_AAF72379	481	AAGACTCTGGCCCTACAGCTGCTCCGTGAATGTGCAAGACAAACAAG	GCAAATCTAGGG *****
DNA35639	541	GCCACAGCATAAAACCTTAGAACTCAATGTACTGGTCCCTCCAGCT	CCTCCATCCTGCC *****
P_AAF72379	541	GCCACAGCATAAAACCTTAGAACTCAATGTACTGGTCCCTCCAGCT	CCTCCATCCTGCC *****
DNA35639	601	GTCTCCAGGGTGTGCCCATGTGGGGCAAACGTGACCTGAGCTGCCA	GTCTCCAAGGA *****
P_AAF72379	601	GTCTCCAGGGTGTGCCCATGTGGGGCAAACGTGACCTGAGCTGCCA	GTCTCCAAGGA *****
DNA35639	661	GTAAGCCCGCTGTCCAATACCAGTGGGATCGGCAGCTCCATC	TTCCAGACTTTCTTG *****
P_AAF72379	661	GTAAGCCCGCTGTCCAATACCAGTGGGATCGGCAGCTCCATC	TTCCAGACTTTCTTG *****
DNA35639	721	CACCAGCATTAGATGTCATCCGTGGGTCTTAAGCCTCACCAAC	CTTCTGTCTTCCATGG *****
P_AAF72379	721	CACCAGCATTAGATGTCATCCGTGGGTCTTAAGCCTCACCAAC	CTTCTGTCTTCCATGG *****
DNA35639	781	CTGGAGTCTATGTCAGGCCACAATGAGGTGGGCACTGCCAATG	TAATGTGACGC *****
P_AAF72379	781	CTGGAGTCTATGTCAGGCCACAATGAGGTGGGCACTGCCAATG	TAATGTGACGC *****
DNA35639	841	TGGAAGTGAGCACAGGGCCTGGAGCTGCAGTGGTGCTGGAGC	TGTGGTACCCCTGG *****
P_AAF72379	841	TGGAAGTGAGCACAGGGCCTGGAGCTGCAGTGGTGCTGGAGC	TGTGGTACCCCTGG *****
DNA35639	901	TTGGACTGGGTTGCTGGCTGGCTGGCTCTTGTA	CCACCGCCGGGCAAGGCCCTGG *****
P_AAF72379	901	TTGGACTGGGTTGCTGGCTGGCTGGCTCTTGTA	CCACCGCCGGGCAAGGCCCTGG *****
DNA35639	961	AGGAGCCAGCCAATGATATCAAGGAGGATGCCATTGCT	CCCCGGACCTGCCCTGGGCCCA *****
P_AAF72379	961	AGGAGCCAGCCAATGATATCAAGGAGGATGCCATTGCT	CCCCGGACCTGCCCTGGGCCCA *****
DNA35639	1021	AGAGCTCAGACACAATCTCCAAGAATGGGACCC	TTCCCTCTGTCACCTCCGCACGAGCCC *****
P_AAF72379	1021	AGAGCTCAGACACAATCTCCAAGAATGGGACCC	TTCCCTCTGTCACCTCCGCACGAGCCC *****

BLAST RESULTS A-S

DNA35639	1081	TCCGGCCACCCCATGGCCCTCCCAGGCCTGGTGCATTGACCCCCACGCCAGTCTCTCCA *****
P_AAF72379	1081	TCCGGCCACCCCATGGCCCTCCCAGGCCTGGTGCATTGACCCCCACGCCAGTCTCTCCA
DNA35639	1141	GCCAGGCCCTGCCCTACCAAGACTGCCACGACAGATGGGGCCCACCCCTAACCAATAT *****
P_AAF72379	1141	GCCAGGCCCTGCCCTACCAAGACTGCCACGACAGATGGGGCCCACCCCTAACCAATAT
DNA35639	1201	CCCCCATCCCTGGTGGGTTCTTCCTCTGGCTTGAGCGCATGGGTGCTGTGCCTGTGA *****
P_AAF72379	1201	CCCCCATCCCTGGTGGGTTCTTCCTCTGGCTTGAGCGCATGGGTGCTGTGCCTGTGA
DNA35639	1261	TGGTGCCTGCCAGAGTCAGACTGGCTCTGGTATGATGACCCCACCACTCATTGGCTA *****
P_AAF72379	1261	TGGTGCCTGCCAGAGTCAGACTGGCTCTGGTATGATGACCCCACCACTCATTGGCTA
DNA35639	1321	AAGGATTGGGGTCTCTCCTCTATAAGGGTCACCTCTAGCACAGAGGCCCTGAGTCATG *****
P_AAF72379	1321	AAGGATTGGGGTCTCTCCTCTATAAGGGTCACCTCTAGCACAGAGGCCCTGAGTCATG
DNA35639	1381	GGAAAGAGTCACACTCCTGACCCTTAGTACTCTGCCACCTCTCTTACTGTGGAAA *****
P_AAF72379	1381	GGAAAGAGTCACACTCCTGACCCTTAGTACTCTGCCACCTCTCTTACTGTGGAAA
DNA35639	1441	ACCATCTCAGTAAGACCTAAGTGTCCAGGAGACAGAAGGAGAAGAGGAAGTGGATCTGGA *****
P_AAF72379	1441	ACCATCTCAGTAAGACCTAAGTGTCCAGGAGACAGAAGGAGAAGAGGAAGTGGATCTGGA
DNA35639	1501	ATTGGGAGGAGCCTCCACCCACCCCTGACTCCTCTTATGAAGCCAGTGCTGAAATTAG *****
P_AAF72379	1501	ATTGGGAGGAGCCTCCACCCACCCCTGACTCCTCTTATGAAGCCAGTGCTGAAATTAG
DNA35639	1561	CTACTCACCAAGAGTGAGGGGCAGAGACTTCCAGTCACTGAGTCTCCAGGCCCTTGA *****
P_AAF72379	1561	CTACTCACCAAGAGTGAGGGGCAGAGACTTCCAGTCACTGAGTCTCCAGGCCCTTGA
DNA35639	1621	TCTGTACCCCACCCCTATCTAACACCACCCCTGGCTCCACTCCAGCTCCCTGTATTGAT *****
P_AAF72379	1621	TCTGTACCCCACCCCTATCTAACACCACCCCTGGCTCCACTCCAGCTCCCTGTATTGAT
DNA35639	1681	ATAACCTGTCAGGCTGGTTAGGTTACTGGGGCAGAGGAATCTCTTAT *****
P_AAF72379	1681	ATAACCTGTCAGGCTGGTTAGGTTACTGGGGCAGAGGAATCTCTTAT
DNA35639	1741	AAAAACTAACATGAAATATGTGTTTCATTTGCAAATTAAATAAGATAACATAATG *****
P_AAF72379	1741	AAAAACTAACATGAAATATGTGTTTCATTTGCAAATTAAATAAGATAACATAATG
DNA35639	1801	TTTGTATGAAAAA *****
P_AAF72379	1801	TTTGTATGAAAAA

>3 P\_AAC87040 Nucleotide sequence of human polypeptide PRO246. (1813 bp) [1 seg]  
 Score = 1813 (3594 bits), Expect = 0.0  
 Identities = 1813/1813 (100%), at 1,1-1813,1813, Strand +/-

BLAST RESULTS A-J

DNA35639	1	GGAGCCGCCCTGGGTGTCAGCGGCTCGGCTCCGCACGCTCCGGCGTCGCGCAGCCT *****
P_AAC87040	1	GGAGCCGCCCTGGGTGTCAGCGGCTCGGCTCCGCACGCTCCGGCGTCGCGCAGCCT
DNA35639	61	CGGCACCTGCAGGTCCGTGCGTCCC CGGGCTGGCGCCCTGACTCCGTCCGGCCAGGGA *****
P_AAC87040	61	CGGCACCTGCAGGTCCGTGCGTCCC CGGGCTGGCGCCCTGACTCCGTCCGGCCAGGGA
DNA35639	121	GGGCCATGATTCCCTCCC GGGGCCCTGGTGACCAACTTGCTGCGGTTTTGTTCTGG *****
P_AAC87040	121	GGGCCATGATTCCCTCCC GGGGCCCTGGTGACCAACTTGCTGCGGTTTTGTTCTGG
DNA35639	181	GGCTGAGTGCCTCGCGCCCCCTCGCGGGCCAGCTGCAACTGCAC TTGCCGCCAAC *****
P_AAC87040	181	GGCTGAGTGCCTCGCGCCCCCTCGCGGGCCAGCTGCAACTGCAC TTGCCGCCAAC
DNA35639	241	GGTTGCAGGCGGTGGAGGGAGGGAAAGTGGTGCTTCCAGCGTGGTACACCTGCACGGGG *****
P_AAC87040	241	GGTTGCAGGCGGTGGAGGGAGGGAAAGTGGTGCTTCCAGCGTGGTACACCTGCACGGGG
DNA35639	301	AGGTGTCTTCATCCCAGCCATGGGAGGTGCCCTTGTGATGTGGTTCTTCAAACAGAAAG *****
P_AAC87040	301	AGGTGTCTTCATCCCAGCCATGGGAGGTGCCCTTGTGATGTGGTTCTTCAAACAGAAAG
DNA35639	361	AAAAGGAGGATCAGGTGTTGCTCACATCAATGGGTCACAACAAGCAAACCTGGAGTAT *****
P_AAC87040	361	AAAAGGAGGATCAGGTGTTGCTCACATCAATGGGTCACAACAAGCAAACCTGGAGTAT
DNA35639	421	CCTTGGTCTACTCCATGCCCTCCCGAACCTGTCCTCGGGCTGGAGGGTCTCCAGGAGA *****
P_AAC87040	421	CCTTGGTCTACTCCATGCCCTCCCGAACCTGTCCTCGGGCTGGAGGGTCTCCAGGAGA
DNA35639	481	AAGACTCTGGCCCTACAGCTGCTCCGTGAATGTGCAAGACAAACAAGGAAATCTAGGG *****
P_AAC87040	481	AAGACTCTGGCCCTACAGCTGCTCCGTGAATGTGCAAGACAAACAAGGAAATCTAGGG
DNA35639	541	GCCACAGCATAAAACCTTAGAACTCAATGTACTGGTTCCCTCAGCTCCATCCTGCC *****
P_AAC87040	541	GCCACAGCATAAAACCTTAGAACTCAATGTACTGGTTCCCTCAGCTCCATCCTGCC
DNA35639	601	GTCTCCAGGGTGTGCCCATGTGGGGCAAACGTGACCTGAGCTGCCAGTCTCCAAGGA *****
P_AAC87040	601	GTCTCCAGGGTGTGCCCATGTGGGGCAAACGTGACCTGAGCTGCCAGTCTCCAAGGA
DNA35639	661	GTAAGCCGCTGTCCAATACCAGTGGGATCGGCAGCTCCATCCTCCAGACTTCTTG *****
P_AAC87040	661	GTAAGCCGCTGTCCAATACCAGTGGGATCGGCAGCTCCATCCTCCAGACTTCTTG
DNA35639	721	CACCAGCATTAGATGTCATCCGTGGTCTTAAGCCTCACCAACCTTCGTCTCCATGG *****
P_AAC87040	721	CACCAGCATTAGATGTCATCCGTGGTCTTAAGCCTCACCAACCTTCGTCTCCATGG
DNA35639	781	CTGGAGTCTATGTCAGCGGCCACAATGAGGTGGGACTGCCAATGTAATGTGACGC *****
P_AAC87040	781	CTGGAGTCTATGTCAGCGGCCACAATGAGGTGGGACTGCCAATGTAATGTGACGC
DNA35639	841	TGGAAGTGAGCACAGGGCCTGGAGCTGCAGTGGTTGCTGGAGCTGTTGGTACCTGG

Blast results A-T

P\_AAC87040 841 TGGAAGTGAGCACAGGGCTGGAGCTGCAGTGGTGTGGAGCTGTTGTGGGTACCCCTGG  
DNA35639 901 TTGGACTGGGTTGCTGGCTGGCCTGGTCTTGTACCACCGCCGGGCAAGGCCCTGG  
P\_AAC87040 901 TTGGACTGGGTTGCTGGCTGGCCTGGTCTTGTACCACCGCCGGGCAAGGCCCTGG  
DNA35639 961 AGGAGCCAGCCAATGATATCAAGGAGGATGCCATTGCTCCCCGGACCCTGCCCTGGCCCA  
P\_AAC87040 961 AGGAGCCAGCCAATGATATCAAGGAGGATGCCATTGCTCCCCGGACCCTGCCCTGGCCCA  
DNA35639 1021 AGAGCTCAGACACAATCTCCAAGAATGGGACCCTTCCTCTGTCACCTCCGACAGGCC  
P\_AAC87040 1021 AGAGCTCAGACACAATCTCCAAGAATGGGACCCTTCCTCTGTCACCTCCGACAGGCC  
DNA35639 1081 TCCGGCCACCCCATGGCCCTCCCAGGCCTGGTGCATTGACCCCCACGCCAGTCTCTCCA  
P\_AAC87040 1081 TCCGGCCACCCCATGGCCCTCCCAGGCCTGGTGCATTGACCCCCACGCCAGTCTCTCCA  
DNA35639 1141 GCCAGGCCCTGCCCTCACCAAGACTGCCACGACAGATGGGGCCACCCCTAACCAATAT  
P\_AAC87040 1141 GCCAGGCCCTGCCCTCACCAAGACTGCCACGACAGATGGGGCCACCCCTAACCAATAT  
DNA35639 1201 CCCCCATCCCTGGTGGGTTCTCCTCTGGCTTGAGCCGCATGGGTGCTGTGCCTGTGA  
P\_AAC87040 1201 CCCCCATCCCTGGTGGGTTCTCCTCTGGCTTGAGCCGCATGGGTGCTGTGCCTGTGA  
DNA35639 1261 TGGTGCCTGCCAGAGTCAGACTGGCTCTGGTATGATGACCCCCACCACTCATTGGCTA  
P\_AAC87040 1261 TGGTGCCTGCCAGAGTCAGACTGGCTCTGGTATGATGACCCCCACCACTCATTGGCTA  
DNA35639 1321 AAGGATTGGGTCTCTCCTTCTATAAGGGTCACCTCTAGCACAGAGGCCCTGAGTCATG  
P\_AAC87040 1321 AAGGATTGGGTCTCTCCTTCTATAAGGGTCACCTCTAGCACAGAGGCCCTGAGTCATG  
DNA35639 1381 GGAAAGAGTCACACTCCTGACCCCTAGTACTCTGCCACCTCTTACTGTGGAAA  
P\_AAC87040 1381 GGAAAGAGTCACACTCCTGACCCCTAGTACTCTGCCACCTCTTACTGTGGAAA  
DNA35639 1441 ACCATCTCAGTAAGACCTAACAGTGTCCAGGAGACAGAAGGGAGAGGAAGTGGATCTGGA  
P\_AAC87040 1441 ACCATCTCAGTAAGACCTAACAGTGTCCAGGAGACAGAAGGGAGAGGAAGTGGATCTGGA  
DNA35639 1501 ATTGGGAGGAGCCTCCACCCACCCCTGACTCCTCTTATGAAGCCAGCTGCTGAAATTAG  
P\_AAC87040 1501 ATTGGGAGGAGCCTCCACCCACCCCTGACTCCTCTTATGAAGCCAGCTGCTGAAATTAG  
DNA35639 1561 CTACTCACCAAGAGTGAGGGCAGAGACTTCCAGTCAGTCACTGAGTCTCCAGGCCCTTGA  
P\_AAC87040 1561 CTACTCACCAAGAGTGAGGGCAGAGACTTCCAGTCAGTCACTGAGTCTCCAGGCCCTTGA  
DNA35639 1621 TCTGTACCCACCCCTATCTAACACCACCCCTGGCTCCACTCCAGCTCCCTGTATTGAT  
P\_AAC87040 1621 TCTGTACCCACCCCTATCTAACACCACCCCTGGCTCCACTCCAGCTCCCTGTATTGAT  
DNA35639 1681 ATAACCTGTCAGGCTGGCTTGGTAGGTTACTGGGGCAGAGGAATCTCTTAT

BLAST RESULTS A-6

P\_AAC87040 1681 ATAACCTGTCAGGCTGGCTGGTTAGGTTACTGGGCAGAGGAATCTCTTAT  
DNA35639 1741 TAAAACATAACATGAAATATGTGTTGTTCAATTGCAAATTAAATAAGATAACATAATG  
\*\*\*\*\*  
P\_AAC87040 1741 TAAAACATAACATGAAATATGTGTTGTTCAATTGCAAATTAAATAAGATAACATAATG  
DNA35639 1801 TTTGTATGAAAAA  
\*\*\*\*\*  
P\_AAC87040 1801 TTTGTATGAAAAA  
  
>4 P\_AAF60372 PRO246 coding sequence. (1813 bp) [1 seg]  
Score = 1813 (3594 bits), Expect = 0.0  
Identities = 1813/1813 (100%), at 1,1-1813,1813, Strand +/  
  
DNA35639 1 GGAGCCGCCCTGGGTGTCAGCGGCTCGGCTCCCGCGCACGCTCCGGCCGTCGCGCAGCCT  
\*\*\*\*\*  
P\_AAF60372 1 GGAGCCGCCCTGGGTGTCAGCGGCTCGGCTCCCGCGCACGCTCCGGCCGTCGCGCAGCCT  
DNA35639 61 CGGCACCTGCAGGTCCGTGCGTCCCGCGGCTGGCCCCCTGACTCCGTCCCGGCCAGGGA  
\*\*\*\*\*  
P\_AAF60372 61 CGGCACCTGCAGGTCCGTGCGTCCCGCGGCTGGCCCCCTGACTCCGTCCCGGCCAGGGA  
DNA35639 121 GGGCCATGATTCCCTCCCAGGGGCCCTGGTGACCAACTTGCTGCGGTTTTGTTCTGG  
\*\*\*\*\*  
P\_AAF60372 121 GGGCCATGATTCCCTCCCAGGGGCCCTGGTGACCAACTTGCTGCGGTTTTGTTCTGG  
DNA35639 181 GGCTGAGTGCCTCGCGCCCCCTCGCGGGCCAGCTGCAACTGCACTTGCCCCGCCAAC  
\*\*\*\*\*  
P\_AAF60372 181 GGCTGAGTGCCTCGCGCCCCCTCGCGGGCCAGCTGCAACTGCACTTGCCCCGCCAAC  
DNA35639 241 GGTTGCAGGCAGGTGGAGGGAGGGAGGGAAAGTGGTGCTTCCAGCGTGGTACACCTGCACGGGG  
\*\*\*\*\*  
P\_AAF60372 241 GGTTGCAGGCAGGTGGAGGGAGGGAAAGTGGTGCTTCCAGCGTGGTACACCTGCACGGGG  
DNA35639 301 AGGTGTCTTCATCCCAGCCATGGGAGGTGCCCTTGTGATGTGGTCTTCAAACAGAAAG  
\*\*\*\*\*  
P\_AAF60372 301 AGGTGTCTTCATCCCAGCCATGGGAGGTGCCCTTGTGATGTGGTCTTCAAACAGAAAG  
DNA35639 361 AAAAGGAGGATCAGGTGTTGCTACATCAATGGGGTCACAACAAGCAAACCTGGAGTAT  
\*\*\*\*\*  
P\_AAF60372 361 AAAAGGAGGATCAGGTGTTGCTACATCAATGGGGTCACAACAAGCAAACCTGGAGTAT  
DNA35639 421 CCTTGGTCTACTCCATGCCCTCCCGAACCTGTCCCTGCGCTGGAGGGCTCCAGGAGA  
\*\*\*\*\*  
P\_AAF60372 421 CCTTGGTCTACTCCATGCCCTCCCGAACCTGTCCCTGCGCTGGAGGGCTCCAGGAGA  
DNA35639 481 AAGACTCTGGCCCTACAGCTGCTCCGTGAATGTGCAAGACAAACAAGGAAATCTAGGG  
\*\*\*\*\*  
P\_AAF60372 481 AAGACTCTGGCCCTACAGCTGCTCCGTGAATGTGCAAGACAAACAAGGAAATCTAGGG  
DNA35639 541 GCCACAGCATAAAACCTTAGAACTCAATGTACTGGTTCCCTCAGCTCCATCCTGCC  
\*\*\*\*\*  
P\_AAF60372 541 GCCACAGCATAAAACCTTAGAACTCAATGTACTGGTTCCCTCAGCTCCATCCTGCC  
DNA35639 601 GTCTCCAGGGTGTGCCCATGTGGGGCAAACGTGACCCCTGAGCTGCCAGTCTCCAAGGA  
\*\*\*\*\*  
P\_AAF60372 601 GTCTCCAGGGTGTGCCCATGTGGGGCAAACGTGACCCCTGAGCTGCCAGTCTCCAAGGA

*BLAST RESULTS A9*

DNA35639	661	GTAAGCCCGCTGTCCAATACCAGTGGGATCGGCAGCTCCATCCTTCAGACTTTCTTG *****
P_AAF60372	661	GTAAGCCCGCTGTCCAATACCAGTGGGATCGGCAGCTCCATCCTTCAGACTTTCTTG *****
DNA35639	721	CACCAAGCATTAGATGTCATCCGTGGTCTTAAGCCTCACCAACCTTCGTCTCCATGG *****
P_AAF60372	721	CACCAAGCATTAGATGTCATCCGTGGTCTTAAGCCTCACCAACCTTCGTCTCCATGG *****
DNA35639	781	CTGGAGTCTATGTCTGCAAGGCCACAATGAGGTGGCACTGCCAATGTAATGTGACGC *****
P_AAF60372	781	CTGGAGTCTATGTCTGCAAGGCCACAATGAGGTGGCACTGCCAATGTAATGTGACGC *****
DNA35639	841	TGGAAGTGAGCACAGGCCCTGGAGCTGCAGTGGTGCTGGAGCTGTTGTGGGTACCCCTGG *****
P_AAF60372	841	TGGAAGTGAGCACAGGCCCTGGAGCTGCAGTGGTGCTGGAGCTGTTGTGGGTACCCCTGG *****
DNA35639	901	TTGGACTGGGTTGCTGGCTGGCTGGCTGGCCTTGTACCAACGCCGGGCAAGGCCCTGG *****
P_AAF60372	901	TTGGACTGGGTTGCTGGCTGGCTGGCCTTGTACCAACGCCGGGCAAGGCCCTGG *****
DNA35639	961	AGGAGCCAGCCAATGATATCAAGGAGGATGCCATTGCTCCCCGACCCCTGCCCTGGCCA *****
P_AAF60372	961	AGGAGCCAGCCAATGATATCAAGGAGGATGCCATTGCTCCCCGACCCCTGCCCTGGCCA *****
DNA35639	1021	AGAGCTCAGACACAATCTCCAAGAATGGGACCCCTTCCTCTGTCACCTCCGCACGAGCCC *****
P_AAF60372	1021	AGAGCTCAGACACAATCTCCAAGAATGGGACCCCTTCCTCTGTCACCTCCGCACGAGCCC *****
DNA35639	1081	TCCGGCCACCCCATGGCCCTCCCAGGCCTGGTGCATTGACCCCCACGCCAGTCTCTCCA *****
P_AAF60372	1081	TCCGGCCACCCCATGGCCCTCCCAGGCCTGGTGCATTGACCCCCACGCCAGTCTCTCCA *****
DNA35639	1141	GCCAGGCCCTGCCCTCACCAAGACTGCCACGACAGATGGGGCCACCCCTAACCAATAT *****
P_AAF60372	1141	GCCAGGCCCTGCCCTCACCAAGACTGCCACGACAGATGGGGCCACCCCTAACCAATAT *****
DNA35639	1201	CCCCCATCCCTGGTGGGTTCTCCTCTGGCTGAGCCGCATGGTGCTGTGCCTGTGA *****
P_AAF60372	1201	CCCCCATCCCTGGTGGGTTCTCCTCTGGCTGAGCCGCATGGTGCTGTGCCTGTGA *****
DNA35639	1261	TGGTGCCTGCCAGAGTCAGCTGGCTCTGGTATGATGACCCACCACTCATTGGCTA *****
P_AAF60372	1261	TGGTGCCTGCCAGAGTCAGCTGGCTCTGGTATGATGACCCACCACTCATTGGCTA *****
DNA35639	1321	AAGGATTGGGTCTCCTCTATAAGGGTCACCTCTAGCACAGAGGCCCTGAGTCATG *****
P_AAF60372	1321	AAGGATTGGGTCTCCTCTATAAGGGTCACCTCTAGCACAGAGGCCCTGAGTCATG *****
DNA35639	1381	GGAAAGAGTCACACTCCTGACCCCTAGTACTCTGCCACCTCTCTTTACTGTGGAAA *****
P_AAF60372	1381	GGAAAGAGTCACACTCCTGACCCCTAGTACTCTGCCACCTCTCTTTACTGTGGAAA *****
DNA35639	1441	ACCATCTCAGTAAGACCTAAGTGTCCAGGAGACAGAAGGAGAAGAGGAAGTGGATCTGGA *****
P_AAF60372	1441	ACCATCTCAGTAAGACCTAAGTGTCCAGGAGACAGAAGGAGAAGAGGAAGTGGATCTGGA *****

**BLAST RESULTS A-10**

DNA35639 1501 ATTGGGAGGAGCCTCCACCCACCCCTGACTCCTCCTTATGAAGCCAGCTGCTGAAATTAG  
\*\*\*\*\*  
P\_AAF60372 1501 ATTGGGAGGAGCCTCCACCCACCCCTGACTCCTCCTTATGAAGCCAGCTGCTGAAATTAG  
  
DNA35639 1561 CTACTCACCAAGAGTGAGGGGCAGAGACTTCAGTCAGTGAGTCTCCCAGGCCCTTGA  
\*\*\*\*\*  
P\_AAF60372 1561 CTACTCACCAAGAGTGAGGGGCAGAGACTTCAGTCAGTGAGTCTCCCAGGCCCTTGA  
  
DNA35639 1621 TCTGTACCCCACCCCTATCTAACACCACCCCTGGCTCCACTCCAGCTCCCTGTATTGAT  
\*\*\*\*\*  
P\_AAF60372 1621 TCTGTACCCCACCCCTATCTAACACCACCCCTGGCTCCACTCCAGCTCCCTGTATTGAT  
  
DNA35639 1681 ATAACCTGTCAGGCTGGTTAGGTTACTGGGCAGAGGATAGGAAATCTCTTAT  
\*\*\*\*\*  
P\_AAF60372 1681 ATAACCTGTCAGGCTGGTTAGGTTACTGGGCAGAGGATAGGAAATCTCTTAT  
  
DNA35639 1741 TAAAACTAACATGAAATATGTGTTTTCAATTGCAAATTAAATAAGATACTAAATG  
\*\*\*\*\*  
P\_AAF60372 1741 TAAAACTAACATGAAATATGTGTTTTCAATTGCAAATTAAATAAGATACTAAATG  
  
DNA35639 1801 TTTGTATGAAAAA  
\*\*\*\*\*  
P\_AAF60372 1801 TTTGTATGAAAAA  
  
>5 P\_AAA30052 Human PRO246 nucleotide sequence. (1813 bp) [1 seg]  
Score = 1813 (3594 bits), Expect = 0.0  
Identities = 1813/1813 (100%), at 1,1-1813,1813, Strand +/  
  
DNA35639 1 GGAGCCGCCCTGGGTGTCAGCGCTCGGCTCCCGCGCACGCTCCGGCCGTGCGCAGCCT  
\*\*\*\*\*  
P\_AAA30052 1 GGAGCCGCCCTGGGTGTCAGCGCTCGGCTCCCGCGCACGCTCCGGCCGTGCGCAGCCT  
  
DNA35639 61 CGGCACCTGCAGGTCCGTGCGTCCCGCGCTGGCGCCCTGACTCCGTCCGGCCAGGGA  
\*\*\*\*\*  
P\_AAA30052 61 CGGCACCTGCAGGTCCGTGCGTCCCGCGCTGGCGCCCTGACTCCGTCCGGCCAGGGA  
  
DNA35639 121 GGGCCATGATTCCCTCCGGGCCCCCTGGTGACCAACTTGCTGCGGTTTGTTCCTGG  
\*\*\*\*\*  
P\_AAA30052 121 GGGCCATGATTCCCTCCGGGCCCCCTGGTGACCAACTTGCTGCGGTTTGTTCCTGG  
  
DNA35639 181 GGCTGAGTGCCCTCGGCCCGCCAGCTGCAACTGCACTTGCCCCGCCAAC  
\*\*\*\*\*  
P\_AAA30052 181 GGCTGAGTGCCCTCGGCCCGCCAGCTGCAACTGCACTTGCCCCGCCAAC  
  
DNA35639 241 GGTTGCAGGCAGGTGGAGGGAGGGAAAGTGGTGCTTCCAGCGTGGTACACCTGCACGGGG  
\*\*\*\*\*  
P\_AAA30052 241 GGTTGCAGGCAGGTGGAGGGAGGGAAAGTGGTGCTTCCAGCGTGGTACACCTGCACGGGG  
  
DNA35639 301 AGGTGTCTTCATCCCAGCCATGGGAGGTGCCCTTGTGATGTGGTTCTCAAACAGAAAG  
\*\*\*\*\*  
P\_AAA30052 301 AGGTGTCTTCATCCCAGCCATGGGAGGTGCCCTTGTGATGTGGTTCTCAAACAGAAAG  
  
DNA35639 361 AAAAGGAGGATCAGGTGTTGCTACATCAATGGGTACAACAAGCAAACCTGGAGTAT  
\*\*\*\*\*  
P\_AAA30052 361 AAAAGGAGGATCAGGTGTTGCTACATCAATGGGTACAACAAGCAAACCTGGAGTAT  
  
DNA35639 421 CCTTGGTCTACTCCATGCCCTCCCGAACCTGTCCCTGCGGCTGGAGGGTCTCCAGGAGA

BLAST RESULTS A-II

		*****
P_AAA30052	421	CCTTGGTCTACTCCATGCCCTCCCGAACCTGTCCTGCGGCTGGAGGGCTCCAGGAGA
DNA35639	481	AAGACTCTGGCCCCTACAGCTGCTCCGTGAATGTGCAAGACAAACAAGGCAAATCTAGGG
P_AAA30052	481	AAGACTCTGGCCCCTACAGCTGCTCCGTGAATGTGCAAGACAAACAAGGCAAATCTAGGG
DNA35639	541	GCCACAGCATCAAAACCTTAGAACTCAATGTAUTGGTTCCCTCCAGCTCCTCCATCCTGCC
P_AAA30052	541	GCCACAGCATCAAAACCTTAGAACTCAATGTAUTGGTTCCCTCCAGCTCCTCCATCCTGCC
DNA35639	601	GTCTCCAGGGTGTGCCCCATGTGGGGCAAACGTGACCTGAGCTGCCAGTCTCCAAGGA
P_AAA30052	601	GTCTCCAGGGTGTGCCCCATGTGGGGCAAACGTGACCTGAGCTGCCAGTCTCCAAGGA
DNA35639	661	GTAAGCCCCTGTCCAATACCAGTGGGATCGGCAGCTCCATCCTCCAGACTTCTTTG
P_AAA30052	661	GTAAGCCCCTGTCCAATACCAGTGGGATCGGCAGCTCCATCCTCCAGACTTCTTTG
DNA35639	721	CACCAGCATTAGATGTCATCCGTGGTCTTAAGCCTCACCAACCTTCGTCTTCCATGG
P_AAA30052	721	CACCAGCATTAGATGTCATCCGTGGTCTTAAGCCTCACCAACCTTCGTCTTCCATGG
DNA35639	781	CTGGAGTCTATGTCAGGCCACAATGAGGTGGGACTGCCAATGTAATGTGACGC
P_AAA30052	781	CTGGAGTCTATGTCAGGCCACAATGAGGTGGGACTGCCAATGTAATGTGACGC
DNA35639	841	TGGAAGTGAGCACAGGGCCTGGAGCTGCAGTGGTGTGGAGCTGTTGGTACCCCTGG
P_AAA30052	841	TGGAAGTGAGCACAGGGCCTGGAGCTGCAGTGGTGTGGAGCTGTTGGTACCCCTGG
DNA35639	901	TTGGACTGGGTTGCTGGCTGGCTGGCCTCTTGATACCACGCCGGGGCAAGGCCCTGG
P_AAA30052	901	TTGGACTGGGTTGCTGGCTGGCCTCTTGATACCACGCCGGGGCAAGGCCCTGG
DNA35639	961	AGGAGCCAGCCAATGATATCAAGGAGGATGCCATTGCTCCCCGACCTGCCCTGGCCCA
P_AAA30052	961	AGGAGCCAGCCAATGATATCAAGGAGGATGCCATTGCTCCCCGACCTGCCCTGGCCCA
DNA35639	1021	AGAGCTCAGACACAATCTCCAAGAACGGGACCCCTTCCTCTGTCACCTCCGCACGAGCCC
P_AAA30052	1021	AGAGCTCAGACACAATCTCCAAGAACGGGACCCCTTCCTCTGTCACCTCCGCACGAGCCC
DNA35639	1081	TCCGGCCACCCATGGCCCTCCCAGGCCTGGTGCATTGACCCCCACGCCAGTCTCTCCA
P_AAA30052	1081	TCCGGCCACCCATGGCCCTCCCAGGCCTGGTGCATTGACCCCCACGCCAGTCTCTCCA
DNA35639	1141	GCCAGGCCCTGCCCTACCAAGACTGCCACGACAGATGGGGCCACCCCTAACCAATAT
P_AAA30052	1141	GCCAGGCCCTGCCCTACCAAGACTGCCACGACAGATGGGGCCACCCCTAACCAATAT
DNA35639	1201	CCCCCATCCCTGGTGGGTTCTCCTCTGGCTTGAGCCGCATGGTGCTGTGCCTGTGA
P_AAA30052	1201	CCCCCATCCCTGGTGGGTTCTCCTCTGGCTTGAGCCGCATGGTGCTGTGCCTGTGA
DNA35639	1261	TGGTGCCTGCCAGAGTCAGACTGGCTCTGGTATGATGACCCCCACCACTATTGGCTA

A-17

BLAST RESULTS

P\_AAA30052 1261 TGGTGCCTGCCAGAGTCAGCTGGCTCTGGTATGATGACCCCACCACTCATTGGCTA  
DNA35639 1321 AAGGATTGGGTCTCTCCTCCTATAAGGGTCACCTCTAGCACAGAGGCCTGAGTCATG  
\*\*\*\*\*  
P\_AAA30052 1321 AAGGATTGGGTCTCTCCTCCTATAAGGGTCACCTCTAGCACAGAGGCCTGAGTCATG  
DNA35639 1381 GGAAAGAGTCACACTCCTGACCCTTAGTACTCTGCCCTCACCTCTTTACTGTGGGAAA  
\*\*\*\*\*  
P\_AAA30052 1381 GGAAAGAGTCACACTCCTGACCCTTAGTACTCTGCCCTCACCTCTTTACTGTGGGAAA  
DNA35639 1441 ACCATCTCAGTAAGACCTAAGTGTCCAGGAGACAGAAGGAGAAGAGGAAGTGGATCTGGA  
\*\*\*\*\*  
P\_AAA30052 1441 ACCATCTCAGTAAGACCTAAGTGTCCAGGAGACAGAAGGAGAAGAGGAAGTGGATCTGGA  
DNA35639 1501 ATTGGGAGGAGCCTCCACCCACCCCTGACTCCTCTTATGAAGCCAGCTGCTGAAATTAG  
\*\*\*\*\*  
P\_AAA30052 1501 ATTGGGAGGAGCCTCCACCCACCCCTGACTCCTCTTATGAAGCCAGCTGCTGAAATTAG  
DNA35639 1561 CTACTCACCAAGAGTGAGGGGCAGAGACTTCCAGTCACTGAGTCTCCAGGCCCTTGA  
\*\*\*\*\*  
P\_AAA30052 1561 CTACTCACCAAGAGTGAGGGGCAGAGACTTCCAGTCACTGAGTCTCCAGGCCCTTGA  
DNA35639 1621 TCTGTACCCACCCCTATCTAACACCACCCCTGGCTCCACTCCAGCTCCCTGTATTGAT  
\*\*\*\*\*  
P\_AAA30052 1621 TCTGTACCCACCCCTATCTAACACCACCCCTGGCTCCACTCCAGCTCCCTGTATTGAT  
DNA35639 1681 ATAACCTGTCAGGCTGGCTTAGGTTACTGGGCAGAGGATAGGAATCTCTTAT  
\*\*\*\*\*  
P\_AAA30052 1681 ATAACCTGTCAGGCTGGCTTAGGTTACTGGGCAGAGGATAGGAATCTCTTAT  
DNA35639 1741 TAAAACTAACATGAAATATGTGTTCTTACGGCTCCAGCTCCAGCTCCCTGTATTGAT  
\*\*\*\*\*  
P\_AAA30052 1741 TAAAACTAACATGAAATATGTGTTCTTACGGCTCCAGCTCCAGCTCCCTGTATTGAT  
DNA35639 1801 TTTGTATGAAAAA  
\*\*\*\*\*  
P\_AAA30052 1801 TTTGTATGAAAAA

>6 P\_AAX28436 EGF-like homologue PRO246 coding sequence. DNA, PAT 22-JUN-1999  
(1813 bp) [1 seg]  
Score = 1813 (3594 bits), Expect = 0.0  
Identities = 1813/1813 (100%), at 1,1-1813,1813, Strand +/+

DNA35639 1 GGAGCCGCCCTGGGTGTCAGCGGCTCGGCTCCCGCGCACGCTCCGGCGTCGCGCAGCCT  
\*\*\*\*\*  
P\_AAX28436 1 GGAGCCGCCCTGGGTGTCAGCGGCTCGGCTCCCGCGCACGCTCCGGCGTCGCGCAGCCT  
DNA35639 61 CGGCACCTGCAGGTCCGTGCGTCCCGCGGCTGGCGCCCTGACTCCGTCCGGCCAGGGA  
\*\*\*\*\*  
P\_AAX28436 61 CGGCACCTGCAGGTCCGTGCGTCCCGCGGCTGGCGCCCTGACTCCGTCCGGCCAGGGA  
DNA35639 121 GGGCCATGATTCCTCCGGGGCCCTGGTGACCAACTTGCTCGGGTTTGTTCCTGG  
\*\*\*\*\*  
P\_AAX28436 121 GGGCCATGATTCCTCCGGGGCCCTGGTGACCAACTTGCTCGGGTTTGTTCCTGG  
DNA35639 181 GGCTGAGTGCCTCGCGCCCCCTCGCGGGCCAGCTGCAACTGCACTTGCCCGCCAACC  
\*\*\*\*\*

## BLAST RESULTS A-1B

P\_AAX28436 181 GGCTGAGTGCCCTCGC~~CCCC~~CTCGCGGGCCAGCTGCAACTGCAC~~TGCCGCCAAC~~  
DNA35639 241 GGTTGCAGGCGGTGGAGGGAGGGGAAGTGGT~~GCTTCAGCGTGGTACACCTTG~~CACGGGG  
\*\*\*\*\*  
P\_AAX28436 241 GGTTGCAGGCGGTGGAGGGAGGGGAAGTGGT~~GCTTCAGCGTGGTACACCTTG~~CACGGGG  
DNA35639 301 AGGTGTCTTCATCCCAGCCATGGGAGGTGCC~~CTTGATGTGGTCTTCAAACAGAAAG~~  
\*\*\*\*\*  
P\_AAX28436 301 AGGTGTCTTCATCCCAGCCATGGGAGGTGCC~~CTTGATGTGGTCTTCAAACAGAAAG~~  
DNA35639 361 AAAAGGAGGATCAGGT~~GTTGTCCTACATCAATGGGTACAACAAGCAAACCTGGAGTAT~~  
\*\*\*\*\*  
P\_AAX28436 361 AAAAGGAGGATCAGGT~~GTTGTCCTACATCAATGGGTACAACAAGCAAACCTGGAGTAT~~  
DNA35639 421 CCTTGGT~~CTACTCCATGCCCTCCCGAACCTGTCCTGCGGCTGGAGGTCTCCAGGAGA~~  
\*\*\*\*\*  
P\_AAX28436 421 CCTTGGT~~CTACTCCATGCCCTCCCGAACCTGTCCTGCGGCTGGAGGTCTCCAGGAGA~~  
DNA35639 481 AAGACTCTGGCC~~CTACAGCTGCTCCGTGAATGTGCAAGACAAACAAGGCAAATCTAGGG~~  
\*\*\*\*\*  
P\_AAX28436 481 AAGACTCTGGCC~~CTACAGCTGCTCCGTGAATGTGCAAGACAAACAAGGCAAATCTAGGG~~  
DNA35639 541 GCCACAGCAT~~AAAACCTTAGAACTCAATGTACTGGTTCCTCCAGCTCCTCCATCCTGCC~~  
\*\*\*\*\*  
P\_AAX28436 541 GCCACAGCAT~~AAAACCTTAGAACTCAATGTACTGGTTCCTCCAGCTCCTCCATCCTGCC~~  
DNA35639 601 GTCTCCAGGGTGTGCC~~CCATGTGGGGCAAACGTGACCTGAGCTGCCAGTCTCAAGGA~~  
\*\*\*\*\*  
P\_AAX28436 601 GTCTCCAGGGTGTGCC~~CCATGTGGGGCAAACGTGACCTGAGCTGCCAGTCTCAAGGA~~  
DNA35639 661 GTAAGCCGCTGT~~CCAATACCAGTGGATCGCAGCTCCATCCTCCAGACTTCTTTG~~  
\*\*\*\*\*  
P\_AAX28436 661 GTAAGCCGCTGT~~CCAATACCAGTGGATCGCAGCTCCATCCTCCAGACTTCTTTG~~  
DNA35639 721 CACCAGCATTAGATGT~~CATCCGTGGTCTTAAAGCCTCACCAACCTTCTGCTTCCATGG~~  
\*\*\*\*\*  
P\_AAX28436 721 CACCAGCATTAGATGT~~CATCCGTGGTCTTAAAGCCTCACCAACCTTCTGCTTCCATGG~~  
DNA35639 781 CTGGAGTCTATGT~~GCAAGGCCACAAATGAGGTGGGACTGCCAATGTAATGTGACGC~~  
\*\*\*\*\*  
P\_AAX28436 781 CTGGAGTCTATGT~~GCAAGGCCACAAATGAGGTGGGACTGCCAATGTAATGTGACGC~~  
DNA35639 841 TGGAAGTGAGCACAGGGC~~CTGGAGCTGCAGTGGTGTGGAGCTGTTGGTACCCCTGG~~  
\*\*\*\*\*  
P\_AAX28436 841 TGGAAGTGAGCACAGGGC~~CTGGAGCTGCAGTGGTGTGGAGCTGTTGGTACCCCTGG~~  
DNA35639 901 TTGGACTGGGTTG~~CTGGCTGGCTGGCCTCTGTACCAACCGCCGGGAAGGCCCTGG~~  
\*\*\*\*\*  
P\_AAX28436 901 TTGGACTGGGTTG~~CTGGCTGGCCTCTGTACCAACCGCCGGGAAGGCCCTGG~~  
DNA35639 961 AGGAGCCAGCCAATGAT~~ATCAAGGAGGATGCCATTGCTCCCCGGACCCCTGCCCTGGCCCA~~  
\*\*\*\*\*  
P\_AAX28436 961 AGGAGCCAGCCAATGAT~~ATCAAGGAGGATGCCATTGCTCCCCGGACCCCTGCCCTGGCCCA~~  
DNA35639 1021 AGAGCTCAGACACAATCT~~CCAAGGAATGGGACCC~~TTCTGT~~CACCTCCGCACGAGGCC~~  
\*\*\*\*\*  
P\_AAX28436 1021 AGAGCTCAGACACAATCT~~CCAAGGAATGGGACCC~~TTCTGT~~CACCTCCGCACGAGGCC~~

Blast results A-A

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DNA35639 1081 TCCGGCCACCCCATGGCCCTCCCAGGCCTGGTGCATTGACCCCCACGCCAGTCTCTCCA
*****
P_AAX28436 1081 TCCGGCCACCCCATGGCCCTCCCAGGCCTGGTGCATTGACCCCCACGCCAGTCTCTCCA

DNA35639 1141 GCCAGGCCCTGCCCTCACCAAGACTGCCACGACAGATGGGGCCACCCCTAACCAATAT
*****
P_AAX28436 1141 GCCAGGCCCTGCCCTCACCAAGACTGCCACGACAGATGGGGCCACCCCTAACCAATAT

DNA35639 1201 CCCCCATCCCTGGTGGGTTCTTCCTCTGGCTTGAGCCGCATGGGTGCTGTGCCTGTGA
*****
P_AAX28436 1201 CCCCCATCCCTGGTGGGTTCTTCCTCTGGCTTGAGCCGCATGGGTGCTGTGCCTGTGA

DNA35639 1261 TGGTGCCTGCCAGAGTCAGCTGGCTCTGGTATGATGACCCCACCACTCATTGGCTA
*****
P_AAX28436 1261 TGGTGCCTGCCAGAGTCAGCTGGCTCTGGTATGATGACCCCACCACTCATTGGCTA

DNA35639 1321 AAGGATTGGGGTCTCTCCTTCTATAAGGGTCACCTCTAGCACAGAGGCCAGTCATG
*****
P_AAX28436 1321 AAGGATTGGGGTCTCTCCTTCTATAAGGGTCACCTCTAGCACAGAGGCCAGTCATG

DNA35639 1381 GGAAAGAGTCACACTCCTGACCCCTAGTACTCTGCCACCTCTTTACTGTGGAAA
*****
P_AAX28436 1381 GGAAAGAGTCACACTCCTGACCCCTAGTACTCTGCCACCTCTTTACTGTGGAAA

DNA35639 1441 ACCATCTCAGTAAGACCTAAGTGTCCAGGAGACAGAAGGAGAAGAGGAAGTGGATCTGGA
*****
P_AAX28436 1441 ACCATCTCAGTAAGACCTAAGTGTCCAGGAGACAGAAGGAGAAGAGGAAGTGGATCTGGA

DNA35639 1501 ATTGGGAGGAGCCTCACCCACCCCTGACTCCTCCTTATGAAGCCAGCTGCTGAAATTAG
*****
P_AAX28436 1501 ATTGGGAGGAGCCTCACCCACCCCTGACTCCTCCTTATGAAGCCAGCTGCTGAAATTAG

DNA35639 1561 CTACTCACCAAGAGTGAGGGCAGAGACTTCCAGTCACTGAGTCTCCAGGCCCTTGA
*****
P_AAX28436 1561 CTACTCACCAAGAGTGAGGGCAGAGACTTCCAGTCACTGAGTCTCCAGGCCCTTGA

DNA35639 1621 TCTGTACCCCACCCCTATCTAACACCACCCCTGGCTCCACTCCAGCTCCGTATTGAT
*****
P_AAX28436 1621 TCTGTACCCCACCCCTATCTAACACCACCCCTGGCTCCACTCCAGCTCCGTATTGAT

DNA35639 1681 ATAACCTGTCAGGCTGGCTTGGTTAGGTTACTGGGCAGAGGATAGGAATCTCTTAT
*****
P_AAX28436 1681 ATAACCTGTCAGGCTGGCTTGGTTAGGTTACTGGGCAGAGGATAGGAATCTCTTAT

DNA35639 1741 TAAAACATGAAATATGTGTTGTTTCATTGCAAATTAAAGATAACATAATG
*****
P_AAX28436 1741 TAAAACATGAAATATGTGTTGTTTCATTGCAAATTAAAGATAACATAATG

DNA35639 1801 TTTGTATGAAAAAA
*****
P_AAX28436 1801 TTTGTATGAAAAAA

```

>7 P\_AAX52221 Protein PRO246 cDNA clone DNA35639-1172. DNA, PAT 25-JUN-1999  
 (1813 bp) [1 seg]  
 Score = 1813 (3594 bits), Expect = 0.0  
 Identities = 1813/1813 (100%), at 1,1-1813,1813, Strand +/+

BLAST RESULTS A-15

DNA35639	1	GGAGCCGCCCTGGGTGTCAGCGGCTCGGCTCCGCACGCTCCGGCGTCGCGCAGCCT *****
P_AAX52221	1	GGAGCCGCCCTGGGTGTCAGCGGCTCGGCTCCGCACGCTCCGGCGTCGCGCAGCCT *****
DNA35639	61	CGGCACCTGCAGGTCCGTGCGTCCC CGCGCTGGCGCCCGT GACTCCGTCCGGCCAGGGA *****
P_AAX52221	61	CGGCACCTGCAGGTCCGTGCGTCCC CGCGCTGGCGCCCGT GACTCCGTCCGGCCAGGGA *****
DNA35639	121	GGGCCATGATTCCCTCCC GGCGCCCTGGTGACCAACTTGCTGCGGTTTTGTTCTGG *****
P_AAX52221	121	GGGCCATGATTCCCTCCC GGCGCCCTGGTGACCAACTTGCTGCGGTTTTGTTCTGG *****
DNA35639	181	GGCTGAGTGCCCTCGC GCCCCCTCGCGGGCCAGCTGCAACTGCACTTGCCCCGCCAACCC *****
P_AAX52221	181	GGCTGAGTGCCCTCGC GCCCCCTCGCGGGCCAGCTGCAACTGCACTTGCCCCGCCAACCC *****
DNA35639	241	GGTGCGAGGCGGTGGAGGGAGGGAAAGTGGTGCTTCAGCGTGGTACACCTTGCAACGGGG *****
P_AAX52221	241	GGTGCGAGGCGGTGGAGGGAGGGAAAGTGGTGCTTCAGCGTGGTACACCTTGCAACGGGG *****
DNA35639	301	AGGTGTCTTCATCCCAGCCATGGGAGGTGCCCTTGTGATGTGGTCTTCAAACAGAAAG *****
P_AAX52221	301	AGGTGTCTTCATCCCAGCCATGGGAGGTGCCCTTGTGATGTGGTCTTCAAACAGAAAG *****
DNA35639	361	AAAAGGAGGATCAGGTGTTGCTTACATCAATGGGTCACAACAAGCAAACCTGGAGTAT *****
P_AAX52221	361	AAAAGGAGGATCAGGTGTTGCTTACATCAATGGGTCACAACAAGCAAACCTGGAGTAT *****
DNA35639	421	CCTTGGTCTACTCCATGCCCTCCCGAACCTGTCCCTGCGGCTGGAGGGTCTCCAGGAGA *****
P_AAX52221	421	CCTTGGTCTACTCCATGCCCTCCCGAACCTGTCCCTGCGGCTGGAGGGTCTCCAGGAGA *****
DNA35639	481	AAGACTCTGGCCCCTACAGCTGCTCCGTGAATGTGCAAGACAAACAAGGCAAATCTAGGG *****
P_AAX52221	481	AAGACTCTGGCCCCTACAGCTGCTCCGTGAATGTGCAAGACAAACAAGGCAAATCTAGGG *****
DNA35639	541	GCCACAGCATAAAACCTTAGAACTCAATGTACTGGTCCCTCAGCTCCATCCTGCC *****
P_AAX52221	541	GCCACAGCATAAAACCTTAGAACTCAATGTACTGGTCCCTCAGCTCCATCCTGCC *****
DNA35639	601	GTCTCCAGGGTGTGCCCATGTGGGGCAACGTGACCCCTGAGCTGCCAGTCTCCAAGGA *****
P_AAX52221	601	GTCTCCAGGGTGTGCCCATGTGGGGCAACGTGACCCCTGAGCTGCCAGTCTCCAAGGA *****
DNA35639	661	GTAAGCCCGCTGTCAAATACCAGTGGGATCGGCAGCTTCCATCCTCCAGACTTTCTTG *****
P_AAX52221	661	GTAAGCCCGCTGTCAAATACCAGTGGGATCGGCAGCTTCCATCCTCCAGACTTTCTTG *****
DNA35639	721	CACCAGCATTAGATGTCATCCGTGGGTCTTAAGCCTCACCAACCTTCTGTCTTCCATGG *****
P_AAX52221	721	CACCAGCATTAGATGTCATCCGTGGGTCTTAAGCCTCACCAACCTTCTGTCTTCCATGG *****
DNA35639	781	CTGGAGTCTATGTCTGCAAGGCCACAATGAGGTGGCACTGCCAATGTAATGTGACGC *****
P_AAX52221	781	CTGGAGTCTATGTCTGCAAGGCCACAATGAGGTGGCACTGCCAATGTAATGTGACGC *****

# BLAST RESULTS A-16

DNA35639	841	TGGAAGTGAGCACAGGGCTGGAGCTGCAGTGGTGCTGGAGCTGTTGGGTACCCCTGG *****
P_AAX52221	841	TGGAAGTGAGCACAGGGCTGGAGCTGCAGTGGTGCTGGAGCTGTTGGGTACCCCTGG *****
DNA35639	901	TTGGACTGGGTTGCTGGCTGGCTGGCTGGTCCCTTGTACCACCGCCGGGCAAGGCCCTGG *****
P_AAX52221	901	TTGGACTGGGTTGCTGGCTGGCTGGTCCCTTGTACCACCGCCGGGCAAGGCCCTGG *****
DNA35639	961	AGGAGCCAGCCAATGATATCAAGGAGGATGCCATTGCTCCCCGACCTGCCCTGGCCA *****
P_AAX52221	961	AGGAGCCAGCCAATGATATCAAGGAGGATGCCATTGCTCCCCGACCTGCCCTGGCCA *****
DNA35639	1021	AGAGCTCAGACACAATCTCCAAGAATGGGACCCCTTCCTCTGTCACCTCCGCACGAGCCC *****
P_AAX52221	1021	AGAGCTCAGACACAATCTCCAAGAATGGGACCCCTTCCTCTGTCACCTCCGCACGAGCCC *****
DNA35639	1081	TCCGGCCACCCCATGGCCCTCCAGGCCTGGTGCATTGACCCCCACGCCAGTCTCTCCA *****
P_AAX52221	1081	TCCGGCCACCCCATGGCCCTCCAGGCCTGGTGCATTGACCCCCACGCCAGTCTCTCCA *****
DNA35639	1141	GCCAGGCCCTGCCCTCACCAAGACTGCCACGACAGATGGGGCCACCCCTAACCAAATAT *****
P_AAX52221	1141	GCCAGGCCCTGCCCTCACCAAGACTGCCACGACAGATGGGGCCACCCCTAACCAAATAT *****
DNA35639	1201	CCCCCATCCCTGGTGGGTTTCTCCTCTGGCTTGAGCCGCATGGTGCTGTGCCTGTGA *****
P_AAX52221	1201	CCCCCATCCCTGGTGGGTTTCTCCTCTGGCTTGAGCCGCATGGTGCTGTGCCTGTGA *****
DNA35639	1261	TGGTGCCTGCCAGAGTCAGCTGGCTCTGGTATGATGACCCCACCACTCATTGGCTA *****
P_AAX52221	1261	TGGTGCCTGCCAGAGTCAGCTGGCTCTGGTATGATGACCCCACCACTCATTGGCTA *****
DNA35639	1321	AAGGATTGGGTCTCTCCTTCTATAAGGGTCACCTCTAGCACAGAGGCCTGAGTCATG *****
P_AAX52221	1321	AAGGATTGGGTCTCTCCTTCTATAAGGGTCACCTCTAGCACAGAGGCCTGAGTCATG *****
DNA35639	1381	GGAAAGAGTCACACTCCTGACCTTAGTACTCTGCCACCTCTTTACTGTGGAAA *****
P_AAX52221	1381	GGAAAGAGTCACACTCCTGACCTTAGTACTCTGCCACCTCTTTACTGTGGAAA *****
DNA35639	1441	ACCATCTCAGTAAGACCTAAGTGTCCAGGAGACAGAAGGAGAAGAGGAAGTGGATCTGGA *****
P_AAX52221	1441	ACCATCTCAGTAAGACCTAAGTGTCCAGGAGACAGAAGGAGAAGAGGAAGTGGATCTGGA *****
DNA35639	1501	ATTGGGAGGAGCCTCACCCACCCCTGACTCCTCTTATGAAGCCAGCTGCTGAAATTAG *****
P_AAX52221	1501	ATTGGGAGGAGCCTCACCCACCCCTGACTCCTCTTATGAAGCCAGCTGCTGAAATTAG *****
DNA35639	1561	CTACTCACCAAGAGTGAGGGCAGAGACTTCCAGTCACTGAGTCTCCAGGCCCTTGA *****
P_AAX52221	1561	CTACTCACCAAGAGTGAGGGCAGAGACTTCCAGTCACTGAGTCTCCAGGCCCTTGA *****
DNA35639	1621	TCTGTACCCCACCCCTATCTAACACCACCCCTGGCTCCACTCCAGCTCCCTGTATTGAT *****
P_AAX52221	1621	TCTGTACCCCACCCCTATCTAACACCACCCCTGGCTCCACTCCAGCTCCCTGTATTGAT *****
DNA35639	1681	ATAACCTGTCAGGCTGGTTGGTTAGGTTACTGGGGCAGAGGATAGGAAATCTCTTAT

BLAST RESULTS A/T

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*****
P_AAX52221 1681 ATAACCTGTCAGGCTGGCTGGTTAGTTTACTGGGCAGAGGAATCTCTTAT
DNA35639 1741 TAAAACATGAAATATGTGTTGTTTCATTGCAAATTAAAGATACTAATG
*****
P_AAX52221 1741 TAAAACATGAAATATGTGTTGTTTCATTGCAAATTAAAGATACTAATG
DNA35639 1801 TTTGTATGAAAAA
*****
P_AAX52221 1801 TTTGTATGAAAAA

>8 AX076924 Sequence 36 from Patent WO0105836. (1813 bp) [1 seg]
Score = 1813 (3594 bits), Expect = 0.0
Identities = 1813/1813 (100%), at 1,1-1813,1813, Strand +/+
DNA35639 1 GGAGCCGCCCTGGGTGTCAGCGCTCGGCTCCCGCGCACGCTCCGGCCGTCGCGCAGCCT
AX076924 1 GGAGCCGCCCTGGGTGTCAGCGCTCGGCTCCCGCGCACGCTCCGGCCGTCGCGCAGCCT
DNA35639 61 CGGCACCTGCAGGTCGTGCGTCCCAGGCTGGCGCCCTGACTCCGTCCGGCCAGGGA
AX076924 61 CGGCACCTGCAGGTCGTGCGTCCCAGGCTGGCGCCCTGACTCCGTCCGGCCAGGGA
DNA35639 121 GGGCCATGATTCCTCCCTCCGGGCCCCCTGGTGACCAACTTGCTGCGGTTTGTTCCTGG
AX076924 121 GGGCCATGATTCCTCCCTCCGGGCCCCCTGGTGACCAACTTGCTGCGGTTTGTTCCTGG
DNA35639 181 GGCTGAGTGCCTCGCGCCCCCTCGCGGGCCAGCTGCAACTGCACTTGCCGCCAAC
AX076924 181 GGCTGAGTGCCTCGCGCCCCCTCGCGGGCCAGCTGCAACTGCACTTGCCGCCAAC
DNA35639 241 GGTTGCAGGCGGTGGAGGGAGGGGAAGTGGTGTCCAGCGTGGTACACCTTGACCGGGG
AX076924 241 GGTTGCAGGCGGTGGAGGGAGGGGAAGTGGTGTCCAGCGTGGTACACCTTGACCGGGG
DNA35639 301 AGGTGTCTTCATCCCAGCCATGGGAGGTGCCCTTGTGATGTGGTTCTCAAACAGAAAG
AX076924 301 AGGTGTCTTCATCCCAGCCATGGGAGGTGCCCTTGTGATGTGGTTCTCAAACAGAAAG
DNA35639 361 AAAAGGAGGATCAGGTGTTGTCTACATCAATGGGTACAACAAGCAAACCTGGAGTAT
AX076924 361 AAAAGGAGGATCAGGTGTTGTCTACATCAATGGGTACAACAAGCAAACCTGGAGTAT
DNA35639 421 CCTTGGTCTACTCCATGCCCTCCGGAACCTGTCCCTGCGGCTGGAGGGCTCCAGGAGA
AX076924 421 CCTTGGTCTACTCCATGCCCTCCGGAACCTGTCCCTGCGGCTGGAGGGCTCCAGGAGA
DNA35639 481 AAGACTCTGGCCCCTACAGCTGCTCCGTGAATGTGCAAGACAACAAGGCAAATCTAGGG
AX076924 481 AAGACTCTGGCCCCTACAGCTGCTCCGTGAATGTGCAAGACAACAAGGCAAATCTAGGG
DNA35639 541 GCCACAGCATAAAACCTTAGAACTCAATGTACTGGTTCCTCCAGCTCCTCCATCCTGCC
AX076924 541 GCCACAGCATAAAACCTTAGAACTCAATGTACTGGTTCCTCCAGCTCCTCCATCCTGCC
DNA35639 601 GTCTCCAGGGTGTGCCCATGTGGGGCAAACGTGACCCTGAGCTGCCAGTCTCCAAGGA
*****
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Blast results A-10

AX076924	601	GTCTCCAGGGTGTCCCCATGTGGGGCAAACGTGACCCTGAGCTGCCAGTCTCCAAGGA
DNA35639	661	GTAAGCCCCTGTCATACCAATACCAAGTGGGATCGGCAGCTCCATCCTCCAGACTTTCTTG *****
AX076924	661	GTAAGCCCCTGTCATACCAATACCAAGTGGGATCGGCAGCTCCATCCTCCAGACTTTCTTG *****
DNA35639	721	CACCAGCATTAGATGTCATCCGTGGGTCTTAAGCCTCACCAACCTTCGTCTCCATGG *****
AX076924	721	CACCAGCATTAGATGTCATCCGTGGGTCTTAAGCCTCACCAACCTTCGTCTCCATGG *****
DNA35639	781	CTGGAGTCTATGTCAGGCCACAATGAGGTGGGCACTGCCAATGTAATGTGACGC *****
AX076924	781	CTGGAGTCTATGTCAGGCCACAATGAGGTGGGCACTGCCAATGTAATGTGACGC *****
DNA35639	841	TGGAAGTGAGCACAGGGCCTGGAGCTGCAGTGGTGTGGAGCTGTTGTGGTACCCCTGG *****
AX076924	841	TGGAAGTGAGCACAGGGCCTGGAGCTGCAGTGGTGTGGAGCTGTTGTGGTACCCCTGG *****
DNA35639	901	TTGGACTGGGTTGCTGGCTGGCTGGCTGGTCTCTGTACCAACGCCGGGGCAAGGCCCTGG *****
AX076924	901	TTGGACTGGGTTGCTGGCTGGCTGGTCTCTGTACCAACGCCGGGGCAAGGCCCTGG *****
DNA35639	961	AGGAGCCAGCAATGATATCAAGGAGGATGCCATTGCTCCCCGACCCCTGCCCTGGCCCA *****
AX076924	961	AGGAGCCAGCAATGATATCAAGGAGGATGCCATTGCTCCCCGACCCCTGCCCTGGCCCA *****
DNA35639	1021	AGAGCTCAGACACAATCTCAAGAACATGGGACCCCTTCCTCTGTACCTCCGACGAGCCC *****
AX076924	1021	AGAGCTCAGACACAATCTCAAGAACATGGGACCCCTTCCTCTGTACCTCCGACGAGCCC *****
DNA35639	1081	TCCGGCCACCCATGGCCCTCCCAGGCCTGGTCATTGACCCCCACGCCAGTCTCTCCA *****
AX076924	1081	TCCGGCCACCCATGGCCCTCCCAGGCCTGGTCATTGACCCCCACGCCAGTCTCTCCA *****
DNA35639	1141	GCCAGGCCCTGCCCTCACCAAGACTGCCACGACAGATGGGGCCCACCCCTAACCAATAT *****
AX076924	1141	GCCAGGCCCTGCCCTCACCAAGACTGCCACGACAGATGGGGCCCACCCCTAACCAATAT *****
DNA35639	1201	CCCCCATCCCTGGTGGGTTCTTCCTCTGGCTTGAGCCGCATGGTGCTGTGCCTGTGA *****
AX076924	1201	CCCCCATCCCTGGTGGGTTCTTCCTCTGGCTTGAGCCGCATGGTGCTGTGCCTGTGA *****
DNA35639	1261	TGGTGCCTGCCAGAGTCAAGCTGGCTCTGGTATGACCCCCACCACTCATTGGCTA *****
AX076924	1261	TGGTGCCTGCCAGAGTCAAGCTGGCTCTGGTATGACCCCCACCACTCATTGGCTA *****
DNA35639	1321	AAGGATTGGGTCTCTCCTATAAGGGTCACCTCTAGCACAGAGGCCTGAGTCATG *****
AX076924	1321	AAGGATTGGGTCTCTCCTATAAGGGTCACCTCTAGCACAGAGGCCTGAGTCATG *****
DNA35639	1381	GGAAAGAGTCACACTCCTGACCCCTAGTACTCTGCCACCTCTTTACTGTGGAAA *****
AX076924	1381	GGAAAGAGTCACACTCCTGACCCCTAGTACTCTGCCACCTCTTTACTGTGGAAA *****
DNA35639	1441	ACCATCTCAGTAAGACCTAAGTGTCCAGGAGACAGAAGGAGAAGAGGAAGTGGATCTGGA *****
AX076924	1441	ACCATCTCAGTAAGACCTAAGTGTCCAGGAGACAGAAGGAGAAGAGGAAGTGGATCTGGA *****

BLAST RESULTS A-19

DNA35639	1501	ATTGGGAGGGAGCCTCCACCCACCCCTGACTCCTCCTTATGAAGCCAGCTGCTGAAATTAG *****
AX076924	1501	ATTGGGAGGGAGCCTCCACCCACCCCTGACTCCTCCTTATGAAGCCAGCTGCTGAAATTAG *****
DNA35639	1561	CTACTCACCAAGAGTGAGGGGCAGAGACTTCCAGTCAGTCAGTGAGTCTCCCAGGCCCTTGA *****
AX076924	1561	CTACTCACCAAGAGTGAGGGGCAGAGACTTCCAGTCAGTCAGTGAGTCTCCCAGGCCCTTGA *****
DNA35639	1621	TCTGTACCCCACCCCTATCTAACACCACCCCTGGCTCCACTCCAGCTCCCTGTATTGAT *****
AX076924	1621	TCTGTACCCCACCCCTATCTAACACCACCCCTGGCTCCACTCCAGCTCCCTGTATTGAT *****
DNA35639	1681	ATAACCTGTCAGGCTGGTTAGGTTTACTGGGGCAGAGGATAGGAATCTCTTAT *****
AX076924	1681	ATAACCTGTCAGGCTGGTTAGGTTTACTGGGGCAGAGGATAGGAATCTCTTAT *****
DNA35639	1741	TAAAACTAACATGAAATATGTGTTGTTTCATTTGCAAATTAAATAAGATACTAATG *****
AX076924	1741	TAAAACTAACATGAAATATGTGTTGTTTCATTTGCAAATTAAATAAGATACTAATG *****
DNA35639	1801	TTTGTATGAAAAA *****
AX076924	1801	TTTGTATGAAAAA *****

>9 P\_AAF93785 Human cDNA encoding a membrane or secretory protein clone  
PSEC0086. (1821 bp) [1 seg]

Score = 1809 (3586 bits), Expect = 0.0

Identities = 1809/1809 (100%), at 1,12-1809,1820, Strand +/-

DNA35639	1	GGAGCCGCCCTGGGTGTCAGCGCTCGGCTCCCGCGCACGCTCCGGCGTCGCGCAGCCT *****
P_AAF93785	12	GGAGCCGCCCTGGGTGTCAGCGCTCGGCTCCCGCGCACGCTCCGGCGTCGCGCAGCCT *****
DNA35639	61	CGGCACCTGCAGGTCCGTGCGTCCC CGGGCTGGCGCCCTGACTCCGTCCCGGCCAGGGA *****
P_AAF93785	72	CGGCACCTGCAGGTCCGTGCGTCCC CGGGCTGGCGCCCTGACTCCGTCCCGGCCAGGGA *****
DNA35639	121	GGGCCATGATTCCCTCCCGGGCCCTGGTGACCAACTTGCTGCGGTTTGTTGTCCTGG *****
P_AAF93785	132	GGGCCATGATTCCCTCCCGGGCCCTGGTGACCAACTTGCTGCGGTTTGTTGTCCTGG *****
DNA35639	181	GGCTGAGTGCCCTCGCGCCCCCTCGCGGGCCCAGCTGCAACTGCACTTGCCCCGCCAAC *****
P_AAF93785	192	GGCTGAGTGCCCTCGCGCCCCCTCGCGGGCCCAGCTGCAACTGCACTTGCCCCGCCAAC *****
DNA35639	241	GGTTGCAGCGGTGGAGGGAGGGGAAGTGGTGCTTCCAGCGTGGTACACCTGCACGGGG *****
P_AAF93785	252	GGTTGCAGCGGTGGAGGGAGGGGAAGTGGTGCTTCCAGCGTGGTACACCTGCACGGGG *****
DNA35639	301	AGGTGTCTTCATCCCAGCCATGGGAGGTGCCCTTGTGATGTGGTTCTTCAAACAGAAAG *****
P_AAF93785	312	AGGTGTCTTCATCCCAGCCATGGGAGGTGCCCTTGTGATGTGGTTCTTCAAACAGAAAG *****
DNA35639	361	AAAAGGAGGATCAGGTGTTGTCCTACATCAATGGGTCACAACAAGCAAACCTGGAGTAT *****
P_AAF93785	372	AAAAGGAGGATCAGGTGTTGTCCTACATCAATGGGTCACAACAAGCAAACCTGGAGTAT *****

BLAST RESULTS A-20

DNA35639	421	CCTTGGTCTACTCCATGCCCTCCCGAACCTGTCCTGCGGCTGGAGGGCTCCAGGAGA *****
P_AAF93785	432	CCTTGGTCTACTCCATGCCCTCCCGAACCTGTCCTGCGGCTGGAGGGCTCCAGGAGA *****
DNA35639	481	AAGACTCTGGCCCCTACAGCTGCTCCGTGAATGTGCAAGACAAACAAGGCAAATCTAGGG *****
P_AAF93785	492	AAGACTCTGGCCCCTACAGCTGCTCCGTGAATGTGCAAGACAAACAAGGCAAATCTAGGG *****
DNA35639	541	GCCACAGCATAAAACCTTAGAACTCAATGTACTGGTTCCAGCTCCTCCATCCTGCC *****
P_AAF93785	552	GCCACAGCATAAAACCTTAGAACTCAATGTACTGGTTCCAGCTCCTCCATCCTGCC *****
DNA35639	601	GTCTCCAGGGTGTGCCCATGTGGGGCAACAGTGACCTGAGCTGCCAGTCTCCAAGGA *****
P_AAF93785	612	GTCTCCAGGGTGTGCCCATGTGGGGCAACAGTGACCTGAGCTGCCAGTCTCCAAGGA *****
DNA35639	661	GTAAGCCGCTGTCCAATACCAGTGGGATCGGCAGCTCCATCCTCCAGACTTCTTG *****
P_AAF93785	672	GTAAGCCGCTGTCCAATACCAGTGGGATCGGCAGCTCCATCCTCCAGACTTCTTG *****
DNA35639	721	CACCAGCATTAGATGTCATCCGTGGTCTTAAGCCTCACCAACCTTCGTCTCCATGG *****
P_AAF93785	732	CACCAGCATTAGATGTCATCCGTGGTCTTAAGCCTCACCAACCTTCGTCTCCATGG *****
DNA35639	781	CTGGAGTCTATGTCATGCCAACAGGGCCACAATGAGGTGGGACTGCCAATGTAATGTGACGC *****
P_AAF93785	792	CTGGAGTCTATGTCATGCCAACAGGGCCACAATGAGGTGGGACTGCCAATGTAATGTGACGC *****
DNA35639	841	TGGAAGTGAGCACAGGGCCTGGAGCTGCAGTGGTTGCTGGAGCTGTTGGTACCTGG *****
P_AAF93785	852	TGGAAGTGAGCACAGGGCCTGGAGCTGCAGTGGTTGCTGGAGCTGTTGGTACCTGG *****
DNA35639	901	TTGGACTGGGTTGCTGGCTGGCTGGCCTCTTGTACCAACCAGCCGGGGCAAGGCCCTGG *****
P_AAF93785	912	TTGGACTGGGTTGCTGGCTGGCCTCTTGTACCAACCAGCCGGGGCAAGGCCCTGG *****
DNA35639	961	AGGAGCCAGCCAATGATATCAAGGAGGATGCCATTGCTCCCCGGACCCCTGCCCTGGCCCA *****
P_AAF93785	972	AGGAGCCAGCCAATGATATCAAGGAGGATGCCATTGCTCCCCGGACCCCTGCCCTGGCCCA *****
DNA35639	1021	AGAGCTCAGACACAATCTCAAGAACATGGGACCCCTTCCTCTGTCACCTCCGACGAGCCC *****
P_AAF93785	1032	AGAGCTCAGACACAATCTCAAGAACATGGGACCCCTTCCTCTGTCACCTCCGACGAGCCC *****
DNA35639	1081	TCCGGCCACCCATGGCCCTCCAGGCCTGGTCATTGACCCCCACGCCAGTCTCTCCA *****
P_AAF93785	1092	TCCGGCCACCCATGGCCCTCCAGGCCTGGTCATTGACCCCCACGCCAGTCTCTCCA *****
DNA35639	1141	GCCAGGCCCTGCCCTACCAAGACTGCCACGACAGATGGGGCCCACCCCTAACCAATAT *****
P_AAF93785	1152	GCCAGGCCCTGCCCTACCAAGACTGCCACGACAGATGGGGCCCACCCCTAACCAATAT *****
DNA35639	1201	CCCCCATCCCTGGTGGGTTCTCCTCTGGCTTGAGCCGATGGTGCTGTGCCTGTGA *****
P_AAF93785	1212	CCCCCATCCCTGGTGGGTTCTCCTCTGGCTTGAGCCGATGGTGCTGTGCCTGTGA *****

BLAST RESULTS A-21

DNA35639	1261	TGGTGCCTGCCAGAGTCAGACTGGCTCTGGTATGATGACCCCACCACTCATTGGCTA *****
P_AAF93785	1272	TGGTGCCTGCCAGAGTCAGACTGGCTCTGGTATGATGACCCCACCACTCATTGGCTA *****
DNA35639	1321	AAGGATTGGGTCTCTCCTATAAGGGCACCTCTAGCACAGAGGCCTGAGTCATG *****
P_AAF93785	1332	AAGGATTGGGTCTCTCCTATAAGGGCACCTCTAGCACAGAGGCCTGAGTCATG *****
DNA35639	1381	GGAAAGAGTCACACTCCTGACCCTAGTACTCTGCCCCACCTCTTTACTGTGGAAA *****
P_AAF93785	1392	GGAAAGAGTCACACTCCTGACCCTAGTACTCTGCCCCACCTCTTTACTGTGGAAA *****
DNA35639	1441	ACCATCTCAGTAAGACCTAACAGTGTCCAGGAGACAGAAGGAGAAGAGGAAGTGGATCTGGA *****
P_AAF93785	1452	ACCATCTCAGTAAGACCTAACAGTGTCCAGGAGACAGAAGGAGAAGAGGAAGTGGATCTGGA *****
DNA35639	1501	ATTGGGAGGAGCCTCCACCCACCCCTGACTCCTCTTATGAAGCCAGCTGCTGAAATTAG *****
P_AAF93785	1512	ATTGGGAGGAGCCTCCACCCACCCCTGACTCCTCTTATGAAGCCAGCTGCTGAAATTAG *****
DNA35639	1561	CTACTCACCAAGAGTGAGGGGCAGAGACTTCCAGTCAGTCACTGAGTCTCCCAGGCCCTTGA *****
P_AAF93785	1572	CTACTCACCAAGAGTGAGGGGCAGAGACTTCCAGTCAGTCACTGAGTCTCCCAGGCCCTTGA *****
DNA35639	1621	TCTGTACCCACCCCTATCTAACACCACCCCTGGCTCCACTCCAGCTCCCTGTATTGAT *****
P_AAF93785	1632	TCTGTACCCACCCCTATCTAACACCACCCCTGGCTCCACTCCAGCTCCCTGTATTGAT *****
DNA35639	1681	ATAACCTGTCAGGCTGGCTTAGGTTACTGGGGCAGAGGATAGGAATCTCTTAT *****
P_AAF93785	1692	ATAACCTGTCAGGCTGGCTTAGGTTACTGGGGCAGAGGATAGGAATCTCTTAT *****
DNA35639	1741	TAAAACTAACATGAAATATGTGTTTCATTGCAAATTAAATAAGATACTAAATG *****
P_AAF93785	1752	TAAAACTAACATGAAATATGTGTTTCATTGCAAATTAAATAAGATACTAAATG *****
DNA35639	1801	TTTGTATGA *****
P_AAF93785	1812	TTTGTATGA

>10 AX136161 Sequence 83 from Patent EP1067182. (1821 bp) [1 seg]  
Score = 1809 (3586 bits), Expect = 0.0  
Identities = 1809/1809 (100%), at 1,12-1809,1820, Strand +/+

DNA35639	1	GGAGCCGCCCTGGGTGTCAGCGCTCGGCTCCGCACGCTCCGGCCGTCGCGCAGCCT *****
AX136161	12	GGAGCCGCCCTGGGTGTCAGCGCTCGGCTCCGCACGCTCCGGCCGTCGCGCAGCCT *****
DNA35639	61	CGGCACCTGCAGGTCCGTGCGTCCCGCGGCTGGCGCCCTGACTCCGTCCGGCCAGGGA *****
AX136161	72	CGGCACCTGCAGGTCCGTGCGTCCCGCGGCTGGCGCCCTGACTCCGTCCGGCCAGGGA *****
DNA35639	121	GGGCCATGATTCCCTCCGGGGCCCTGGTGACCAACTTGCTGCGGTTTTGTTCCCTGG *****
AX136161	132	GGGCCATGATTCCCTCCGGGGCCCTGGTGACCAACTTGCTGCGGTTTTGTTCCCTGG *****
DNA35639	181	GGCTGAGTGCCTCGCGCCCCCTCGCGGGCCAGCTGCAACTGCACTTGCCCCGCAACC *****

BLAST RESULTS A-22

		*****
AX136161	192	GGCTGAGTGCCTCGGCCCGCCAGCTGCAACTGCACTGCCGCCAACC
DNA35639	241	GGTTGCAGGCAGTGGAGGGAGGGAAAGTGGTGCTTCAGCGTGGTACACCTTGACGGGG
AX136161	252	GGTTGCAGGCAGTGGAGGGAGGGAAAGTGGTGCTTCAGCGTGGTACACCTTGACGGGG
DNA35639	301	AGGTGTCTTCATCCCAGCCATGGGAGGTGCCCTTGTGATGTGGTTCTCAAACAGAAAG
AX136161	312	AGGTGTCTTCATCCCAGCCATGGGAGGTGCCCTTGTGATGTGGTTCTCAAACAGAAAG
DNA35639	361	AAAAGGAGGATCAGGTGTTGTCCTACATCAATGGGGTCACAACAAGCAAACCTGGAGTAT
AX136161	372	AAAAGGAGGATCAGGTGTTGTCCTACATCAATGGGGTCACAACAAGCAAACCTGGAGTAT
DNA35639	421	CCTTGGTCTACTCCATGCCCTCCCGAACCTGTCCCTGCGGCTGGAGGGTCTCAGGAGA
AX136161	432	CCTTGGTCTACTCCATGCCCTCCCGAACCTGTCCCTGCGGCTGGAGGGTCTCAGGAGA
DNA35639	481	AAGACTCTGGCCCTACAGCTGCTCCGTGAATGTGCAAGACAACAAGGCAAATCTAGGG
AX136161	492	AAGACTCTGGCCCTACAGCTGCTCCGTGAATGTGCAAGACAACAAGGCAAATCTAGGG
DNA35639	541	GCCACAGCATAAAACCTTAGAACTCAATGTACTGGTTCCCTCAGCTCCTCCATCCTGCC
AX136161	552	GCCACAGCATAAAACCTTAGAACTCAATGTACTGGTTCCCTCAGCTCCTCCATCCTGCC
DNA35639	601	GTCTCCAGGGTGTGCCCATGTGGGGGCAAACGTGACCTGAGCTGCCAGTCTCCAAGGA
AX136161	612	GTCTCCAGGGTGTGCCCATGTGGGGGCAAACGTGACCTGAGCTGCCAGTCTCCAAGGA
DNA35639	661	GTAAGCCGCTGTCCAATACCAGTGGGATCGGCAGCTCCATCCTCCAGACTTCTTTG
AX136161	672	GTAAGCCGCTGTCCAATACCAGTGGGATCGGCAGCTCCATCCTCCAGACTTCTTTG
DNA35639	721	CACCAGCATTAGATGTCATCCGTGGTCTTAAGCCTCACCAACCTTCGTCTCCATGG
AX136161	732	CACCAGCATTAGATGTCATCCGTGGTCTTAAGCCTCACCAACCTTCGTCTCCATGG
DNA35639	781	CTGGAGTCTATGTCAGGCCACAATGAGGTGGGACTGCCAATGTAATGTGACGC
AX136161	792	CTGGAGTCTATGTCAGGCCACAATGAGGTGGGACTGCCAATGTAATGTGACGC
DNA35639	841	TGGAAGTGAGCACAGGCCCTGGAGCTGCAGTGGTGCTGGAGCTGTTGGTACCCCTGG
AX136161	852	TGGAAGTGAGCACAGGCCCTGGAGCTGCAGTGGTGCTGGAGCTGTTGGTACCCCTGG
DNA35639	901	TTGGACTGGGTTGCTGGCTGGCTGGTCTTGTACCAACCAGCCGGGCAAGGCCCTGG
AX136161	912	TTGGACTGGGTTGCTGGCTGGCTGGTCTTGTACCAACCAGCCGGGCAAGGCCCTGG
DNA35639	961	AGGAGCCAGCCAATGATATCAAGGAGGATGCCATTGCTCCCCGGACCCCTGCCCTGGCCCA
AX136161	972	AGGAGCCAGCCAATGATATCAAGGAGGATGCCATTGCTCCCCGGACCCCTGCCCTGGCCCA
DNA35639	1021	AGAGCTCAGACACAATCTCCAAGAATGGGACCCCTTCCTCTGTCACCTCCGACGAGCCC

AX136161 1032 AGAGCTCAGACACAATCTCCAAGAATGGGACCCTTCCTCTGTCACCTCCGCACGAGCCC  
 DNA35639 1081 TCCGGCCACCCCATGGCCCTCCCAGGCCCTGGTGCATTGACCCCCACGCCAGTCTCTCCA  
 \*\*\*\*\*  
 AX136161 1092 TCCGGCCACCCCATGGCCCTCCCAGGCCCTGGTGCATTGACCCCCACGCCAGTCTCTCCA  
 DNA35639 1141 GCCAGGCCCTGCCCTACCAAGACTGCCACGACAGATGGGGCCACCCCAACCAATAT  
 \*\*\*\*\*  
 AX136161 1152 GCCAGGCCCTGCCCTACCAAGACTGCCACGACAGATGGGGCCACCCCAACCAATAT  
 DNA35639 1201 CCCCCATCCCTGGTGGGGTTCTCCTCTGGCTTGAGCCGCATGGGTGCTGTGCCTGTGA  
 \*\*\*\*\*  
 AX136161 1212 CCCCCATCCCTGGTGGGGTTCTCCTCTGGCTTGAGCCGCATGGGTGCTGTGCCTGTGA  
 DNA35639 1261 TGGTGCCTGCCAGAGTCAGACTGGCTCTGGTATGATGACCCACCACTCATTGGCTA  
 \*\*\*\*\*  
 AX136161 1272 TGGTGCCTGCCAGAGTCAGACTGGCTCTGGTATGATGACCCACCACTCATTGGCTA  
 DNA35639 1321 AAGGATTGGGGTCTCCTCCTATAAGGGTCACCTCTAGCACAGAGGCCCTGAGTCATG  
 \*\*\*\*\*  
 AX136161 1332 AAGGATTGGGGTCTCCTCCTATAAGGGTCACCTCTAGCACAGAGGCCCTGAGTCATG  
 DNA35639 1381 GGAAAGAGTCACACTCCTGACCTTAGTACTCTGCCACCTCTTTACTGTGGAAA  
 \*\*\*\*\*  
 AX136161 1392 GGAAAGAGTCACACTCCTGACCTTAGTACTCTGCCACCTCTTTACTGTGGAAA  
 DNA35639 1441 ACCATCTCAGTAAGACCTAACGTGTCCAGGAGACAGAAGGGAGAAGAGGAAGTGGATCTGGA  
 \*\*\*\*\*  
 AX136161 1452 ACCATCTCAGTAAGACCTAACGTGTCCAGGAGACAGAAGGGAGAAGAGGAAGTGGATCTGGA  
 DNA35639 1501 ATTGGGAGGAGCCTCACCCACCCCTGACTCCTTATGAAGCCAGCTGCTGAAATTAG  
 \*\*\*\*\*  
 AX136161 1512 ATTGGGAGGAGCCTCACCCACCCCTGACTCCTTATGAAGCCAGCTGCTGAAATTAG  
 DNA35639 1561 CTACTCACCAAGAGTGAGGGCAGAGACTCCAGTCAGTGAGTCTCCAGGCCCTGAA  
 \*\*\*\*\*  
 AX136161 1572 CTACTCACCAAGAGTGAGGGCAGAGACTCCAGTCAGTGAGTCTCCAGGCCCTGAA  
 DNA35639 1621 TCTGTACCCCACCCCTATCTAACACCACCCCTGGCTCCACTCCAGCTCCCTGTATTGAT  
 \*\*\*\*\*  
 AX136161 1632 TCTGTACCCCACCCCTATCTAACACCACCCCTGGCTCCACTCCAGCTCCCTGTATTGAT  
 DNA35639 1681 ATAACCTGTCAGGCTGGCTGGTTAGGTTTACTGGGGCAGAGGAATCTCTTAT  
 \*\*\*\*\*  
 AX136161 1692 ATAACCTGTCAGGCTGGCTGGTTAGGTTTACTGGGGCAGAGGAATCTCTTAT  
 DNA35639 1741 TAAAACTAACATGAAATATGTGTTGGTTCTGCAAATTAAATAAGATAACATAATG  
 \*\*\*\*\*  
 AX136161 1752 TAAAACTAACATGAAATATGTGTTGGTTCTGCAAATTAAATAAGATAACATAATG  
 DNA35639 1801 TTTGTATGA  
 \*\*\*\*\*  
 AX136161 1812 TTTGTATGA

>11 P\_AAA23441 cDNA encoding human secreted protein vc51\_1, SEQ ID NO:37. (1954  
 bp) [1 seg]  
 Score = 1806 (3580 bits), Expect = 0.0

BLAST RESULTS A-2A

Identities = 1813/1814 (99%), Gaps = 1/1814 (0%), at 1,13-1813,1826, Strand +/-

DNA35639	1	GGAGCCGCCCTGGGTGTCAGC-GGCTCGGCTCCCGCGCACGCTCCGGCCGTGCGCAGCC *****
P AAA23441	13	GGAGCCGCCCTGGGTGTCAGCGGGCTCGGCTCCCGCGCACGCTCCGGCCGTGCGCAGCC *****
DNA35639	60	TGGCACCTGCAGGTCCGTGCGTCCC GGCTGGCGCCCTGACTCCGCTCCGGCCAGGG *****
P AAA23441	73	TGGCACCTGCAGGTCCGTGCGTCCC GGCTGGCGCCCTGACTCCGCTCCGGCCAGGG *****
DNA35639	120	AGGCCATGATTCCCTCCGGGGCCCTGGTGACCAACTTGCTGCGTTTGTTCCTG *****
P AAA23441	133	AGGCCATGATTCCCTCCGGGGCCCTGGTGACCAACTTGCTGCGTTTGTTCCTG *****
DNA35639	180	GGGCTGAGTGCCCTCGCGCCCCCTCGCGGGCCCAGCTGCAACTGCACTTGCCGCCAAC *****
P AAA23441	193	GGGCTGAGTGCCCTCGCGCCCCCTCGCGGGCCCAGCTGCAACTGCACTTGCCGCCAAC *****
DNA35639	240	CGGTTGCAGCGGTGGAGGGAGGGAAAGTGGTGCTTCCAGCGTGGTACACCTTGACGGG *****
P AAA23441	253	CGGTTGCAGCGGTGGAGGGAGGGAAAGTGGTGCTTCCAGCGTGGTACACCTTGACGGG *****
DNA35639	300	GAGGTGTTTCATCCCAGCCATGGGAGGTGCCCTTGTGATGTGGTTCTCAAACAGAAA *****
P AAA23441	313	GAGGTGTTTCATCCCAGCCATGGGAGGTGCCCTTGTGATGTGGTTCTCAAACAGAAA *****
DNA35639	360	GAAAAGGAGGATCAGGTGTTGCTACATCAATGGGTCACAACAAGCAAACCTGGAGTA *****
P AAA23441	373	GAAAAGGAGGATCAGGTGTTGCTACATCAATGGGTCACAACAAGCAAACCTGGAGTA *****
DNA35639	420	TCCTGGTCTACTCCATGCCCTCCCGAACCTGTCCTGCGGCTGGAGGGTCTCCAGGAG *****
P AAA23441	433	TCCTGGTCTACTCCATGCCCTCCCGAACCTGTCCTGCGGCTGGAGGGTCTCCAGGAG *****
DNA35639	480	AAAGACTCTGGCCCTACAGCTGCTCCGTGAATGTCAAGACAAACAAGGCAAATCTAGG *****
P AAA23441	493	AAAGACTCTGGCCCTACAGCTGCTCCGTGAATGTCAAGACAAACAAGGCAAATCTAGG *****
DNA35639	540	GGCCACAGCATAAAACCTTAGAACTCAATGTACTGGTTCCCTCCAGCTCCATCCTGC *****
P AAA23441	553	GGCCACAGCATAAAACCTTAGAACTCAATGTACTGGTTCCCTCCAGCTCCATCCTGC *****
DNA35639	600	CGTCTCCAGGGTGTGCCCATGTGGGGCAAACGTGACCTGAGCTGCCAGTCTCAAGG *****
P AAA23441	613	CGTCTCCAGGGTGTGCCCATGTGGGGCAAACGTGACCTGAGCTGCCAGTCTCAAGG *****
DNA35639	660	AGTAAGCCCGTGTCCAATACCAGTGGATCGGCAGCTCCATCCTCCAGACTTCTTT *****
P AAA23441	673	AGTAAGCCCGTGTCCAATACCAGTGGATCGGCAGCTCCATCCTCCAGACTTCTTT *****
DNA35639	720	GCACCAGCATTAGATGTCATCCGTGGTCTTAAGCCTCACCAACCTTCGTCTCCATG *****
P AAA23441	733	GCACCAGCATTAGATGTCATCCGTGGTCTTAAGCCTCACCAACCTTCGTCTCCATG *****
DNA35639	780	GCTGGAGTCTATGTCTGCAAGGCCACAATGAGGTGGGACTGCCAATGTAATGTGACG *****
P AAA23441	793	GCTGGAGTCTATGTCTGCAAGGCCACAATGAGGTGGGACTGCCAATGTAATGTGACG *****

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DNA35639	840	CTGGAAGTGAGCACAGGGCCTGGAGCTGCAGTGGTGCTGGAGCTGTTGGGTACCTG *****
P_AAA23441	853	CTGGAAGTGAGCACAGGGCCTGGAGCTGCAGTGGTGCTGGAGCTGTTGGGTACCTG *****
DNA35639	900	GTTGGACTGGGTTGCTGGCTGGCCTGGCCTCTTGTACCACCGCCGGGCAAGGCCCTG *****
P_AAA23441	913	GTTGGACTGGGTTGCTGGCTGGCCTGGCCTCTTGTACCACCGCCGGGCAAGGCCCTG *****
DNA35639	960	GAGGAGCCAGCCAATGATATCAAGGAGGATGCCATTGCTCCCCGGACCCTGCCCTGGCCC *****
P_AAA23441	973	GAGGAGCCAGCCAATGATATCAAGGAGGATGCCATTGCTCCCCGGACCCTGCCCTGGCCC *****
DNA35639	1020	AAGAGCTCAGACACAATCTCAAGAACATGGGACCCCTTCCTCTGTCACCTCCGACGAGCC *****
P_AAA23441	1033	AAGAGCTCAGACACAATCTCAAGAACATGGGACCCCTTCCTCTGTCACCTCCGACGAGCC *****
DNA35639	1080	CTCCGGCCACCCCATGGCCCTCCAGGCCTGGTCATTGACCCCCACGCCAGTCTCTCC *****
P_AAA23441	1093	CTCCGGCCACCCCATGGCCCTCCAGGCCTGGTCATTGACCCCCACGCCAGTCTCTCC *****
DNA35639	1140	AGCCAGGCCCTGCCCTCACCAAGACTGCCACGACAGATGGGCCACCCCTAACCAAATA *****
P_AAA23441	1153	AGCCAGGCCCTGCCCTCACCAAGACTGCCACGACAGATGGGCCACCCCTAACCAAATA *****
DNA35639	1200	TCCCCCATCCCTGGTGGGGTTCTTCCTCTGGCTTGAGCCGCATGGTGCTGTGCCTGTG *****
P_AAA23441	1213	TCCCCCATCCCTGGTGGGGTTCTTCCTCTGGCTTGAGCCGCATGGTGCTGTGCCTGTG *****
DNA35639	1260	ATGGTGCCTGCCAGAGTCAGACTGGCTCTGGTATGATGACCCCACCACTCATTGGCT *****
P_AAA23441	1273	ATGGTGCCTGCCAGAGTCAGACTGGCTCTGGTATGATGACCCCACCACTCATTGGCT *****
DNA35639	1320	AAAGGATTGGGTCTCTCCTTCTATAAGGGTCACCTCTAGCACAGAGGCCCTGAGTCAT *****
P_AAA23441	1333	AAAGGATTGGGTCTCTCCTTCTATAAGGGTCACCTCTAGCACAGAGGCCCTGAGTCAT *****
DNA35639	1380	GGGAAAGAGTCACACTCCTGACCCCTAGTACTCTGCCACCTCTTACTGTGGAA *****
P_AAA23441	1393	GGGAAAGAGTCACACTCCTGACCCCTAGTACTCTGCCACCTCTTACTGTGGAA *****
DNA35639	1440	AACCATCTCAGTAAGACCTAAGTGTCCAGGAGACAGAACGGAGAACAGAACGGATCTGG *****
P_AAA23441	1453	AACCATCTCAGTAAGACCTAAGTGTCCAGGAGACAGAACGGAGAACAGAACGGATCTGG *****
DNA35639	1500	AATTGGGAGGAGCCTCCACCCACCCCTGACTCCTCTTATGAAGCCAGCTGCTGAAATTA *****
P_AAA23441	1513	AATTGGGAGGAGCCTCCACCCACCCCTGACTCCTCTTATGAAGCCAGCTGCTGAAATTA *****
DNA35639	1560	GCTACTCACCAAGAGTGAGGGCAGAGACTTCCAGTCACTGAGTCTCCAGGCCCTTG *****
P_AAA23441	1573	GCTACTCACCAAGAGTGAGGGCAGAGACTTCCAGTCACTGAGTCTCCAGGCCCTTG *****
DNA35639	1620	ATCTGTACCCACCCCTATCTAACACCACCCCTGGCTCCCCTCCAGCTCCCTGTATTGA *****
P_AAA23441	1633	ATCTGTACCCACCCCTATCTAACACCACCCCTGGCTCCCCTCCAGCTCCCTGTATTGA *****

BLAST RESULTS A-219

DNA35639	1680	TATAACCTGTCAGGCTGGCTGGTTAGGTTACTGGGGCAGAGGATAGGAATCTCTTA
P_AAA23441	1693	***** TATAACCTGTCAGGCTGGCTGGTTAGGTTACTGGGGCAGAGGATAGGAATCTCTTA
DNA35639	1740	TTAAAACATAACATGAAATATGTGTTGTTCATTTGCAAATTAAATAAGATACATAAT
P_AAA23441	1753	***** TTAAAACATAACATGAAATATGTGTTGTTCATTTGCAAATTAAATAAGATACATAAT
DNA35639	1800	GTTTGTATGAAAAA
P_AAA23441	1813	***** GTTTGTATGAAAAA

>12 AF361746 Homo sapiens endothelial cell-selective adhesion molecule (ESAM) (1838 bp) [1 seg]  
Score = 1805 (3578 bits), Expect = 0.0  
Identities = 1811/1813 (99%), at 1,14-1813,1826, Strand +/+

DNA35639	1	GGAGCCGCCCTGGGTGTCAGCGCTCGGCTCCCGCGCACGCTCCGGCCGTCGCGCAGCCT
AF361746	14	***** GGAGCCGCCCTGGGTGTCAGCGCTCGGCTCCCGCGCACGCTCCGGCCGTCGCGCAGCCT
DNA35639	61	CGGCACCTGCAGGTCCGTGCGTCCC CGCGCTGGCGCCCTGACTCCGTCCGGCCAGGGA
AF361746	74	***** CGGCACCTGCAGGTCCGTGCGTCCC CGCGCTGGCGCCCTGACTCCGTCCGGCCAGGGA
DNA35639	121	GGGCCATGATTCCCTCCCGGGGCCCTGGTGACCAACTTGCTGCGGTTTTGTTCCCTGG
AF361746	134	***** GGGCCATGATTCCCTCCCGGGGCCCTGGTGACCAACTTGCTGCGGTTTTGTTCCCTGG
DNA35639	181	GGCTGAGTGCCTCGCGCCCCCTCGCGGGCCCAGCTGCAACTGCACTTGCCGCCAAC
AF361746	194	***** GGCTGAGTGCCTCGCGCCCCCTCGCGGGCCCAGCTGCAACTGCACTTGCCGCCAAC
DNA35639	241	GGTTGCAGGCGGTGGAGGGAGGGGAAGTGGTGCTCCAGCGTGGTACACCTTGCACGGGG
AF361746	254	***** GGTTGCAGGCGGTGGAGGGAGGGGAAGTGGTGCTCCAGCGTGGTACACCTTGCACGGGG
DNA35639	301	AGGTGTCTTCATCCCAGCCATGGGAGGTGCCCTTGTGATGTGGTTCTTCAAACAGAAAG
AF361746	314	***** AGGTGTCTTCATCCCAGCCATGGGAGGTGCCCTTGTGATGTGGTTCTTCAAACAGAAAG
DNA35639	361	AAAAGGAGGATCAGGTGTTGTCCTACATCAATGGGTACAACAAGCAAACCTGGAGTAT
AF361746	374	***** AAAAGGAGGATCAGGTGTTGTCCTACATCAATGGGTACAACAAGCAAACCTGGAGTAT
DNA35639	421	CCTTGGTCTACTCCATGCCCTCCCGAACCTGTCCCTGCGCTGGAGGGCTCCAGGAGA
AF361746	434	***** CCTTGGTCTACTCCATGCCCTCCCGAACCTGTCCCTGCGCTGGAGGGCTCCAGGAGA
DNA35639	481	AAGACTCTGGCCCTACAGCTGCTCCGTGAATGTGCAAGACAAACAAGGCAAATCTAGGG
AF361746	494	***** AAGACTCTGGCCCTACAGCTGCTCCGTGAATGTGCAAGACAAACAAGGCAAATCTAGGG
DNA35639	541	GCCACAGCATAAAACCTTAGAACTCAATGTACTGGTCCCTCCAGCTCCTCCATCCTGCC
AF361746	554	***** GCCACAGCATAAAACCTTAGAACTCAATGTACTGGTCCCTCCAGCTCCTCCATCCTGCC

DNA35639	601	GTCTCCAGGGTGTGCCCATGTGGGGCAAACGTGACCCTGAGCTGCCAGTCTCCAAGGA *****
AF361746	614	GTCTCCAGGGTGTGCCCATGTGGGGCAAACGTGACCCTGAGCTGCCAGTCTCCAAGGA *****
DNA35639	661	GTAAGCCCCTGTCCAATACCAGTGGATCGCAGCTTCATCCTCCAGACTTTCTTG *****
AF361746	674	GTAAGCCCCTGTCCAATACCAGTGGATCGCAGCTTCATCCTCCAGACTTTCTTG *****
DNA35639	721	CACCAGCATTAGATGTCATCCGTGGTCTTAAGCCTCACCAACCTTCGTCTTCATGG *****
AF361746	734	CACCAGCATTAGATGTCATCCGTGGTCTTAAGCCTCACCAACCTTCGTCTTCATGG *****
DNA35639	781	CTGGAGTCTATGTCGCAAGGCCACAATGAGGTGGGACTGCCAATGTAATGTGACGC *****
AF361746	794	CTGGAGTCTATGTCGCAAGGCCACAATGAGGTGGGACTGCCAATGTAATGTGACGC *****
DNA35639	841	TGGAAGTGAGCACAGGCCCTGGAGCTGCAGTGGTGTGGAGCTGGTGTGGTACCGCTGG *****
AF361746	854	TGGAAGTGAGCACAGGCCCTGGAGCTGCAGTGGTGTGGAGCTGGTGTGGTACCGCTGG *****
DNA35639	901	TTGGACTGGGTTGCTGGCTGGCTGGTCTCTGTACCAACGCCGGGGCAAGGCCCTGG *****
AF361746	914	TTGGACTGGGTTGCTGGCTGGCTGGTCTCTGTACCAACGCCGGGGCAAGGCCCTGG *****
DNA35639	961	AGGAGCCAGCCAATGATATCAAGGAGGATGCCATTGCTCCCCGACCTGCCCTGGCCCA *****
AF361746	974	AGGAGCCAGCCAATGATATCAAGGAGGATGCCATTGCTCCCCGAACCTGCCCTGGCCCA *****
DNA35639	1021	AGAGCTCAGACACAATCTCAAGAACATGGGACCTTCTGTACCTCCGACGAGCCC *****
AF361746	1034	AGAGCTCAGACACAATCTCAAGAACATGGGACCTTCTGTACCTCCGACGAGCCC *****
DNA35639	1081	TCCGGCCACCCATGGCCCTCCAGGCCTGGTCATTGACCCCCACGCCAGTCTCTCCA *****
AF361746	1094	TCCGGCCACCCATGGCCCTCCAGGCCTGGTCATTGACCCCCACGCCAGTCTCTCCA *****
DNA35639	1141	GCCAGGCCCTGCCCTCACCAAGACTGCCACGACAGATGGGGCCACCTCAACCAATAT *****
AF361746	1154	GCCAGGCCCTGCCCTCACCAAGACTGCCACGACAGATGGGGCCACCTCAACCAATAT *****
DNA35639	1201	CCCCCATCCCTGGTGGGTTCTCCTCTGGCTTGAGCCGCATGGTGCTGTGCCTGTGA *****
AF361746	1214	CCCCCATCCCTGGTGGGTTCTCCTCTGGCTTGAGCCGCATGGTGCTGTGCCTGTGA *****
DNA35639	1261	TGGTGCCTGCCAGAGTCAGCTGGCTCTGGTATGATGACCCCACCACTCATTGGCTA **
AF361746	1274	TGATGCCTGCCAGAGTCAGCTGGCTCTGGTATGATGACCCCACCACTCATTGGCTA *****
DNA35639	1321	AAGGATTGGGTCTCTCCTCTATAAGGGTCACCTCTAGCACAGAGGCCTGAGTCATG *****
AF361746	1334	AAGGATTGGGTCTCTCCTCTATAAGGGTCACCTCTAGCACAGAGGCCTGAGTCATG *****
DNA35639	1381	GGAAAGAGTCACACTCCTGACCTTAGTACTCTGCCACCTCTTACTGTGGAAA *****
AF361746	1394	GGAAAGAGTCACACTCCTGACCTTAGTACTCTGCCACCTCTTACTGTGGAAA *****
DNA35639	1441	ACCATCTCAGTAAGACCTAAGTGTCCAGGAGACAGAAGGAGAAGAGGAAGTGGATCTGGA *****

BLAST RESULTS A-10

```
*****
AF361746 1454 ACCATCTCAGTAAGACCTAAGTGTCCAGGAGACAGAAGGAGAAAGAGGAAGTGGATCTGGA
DNA35639 1501 ATTGGGAGGAGCCTCCACCCACCCCTGACTCCTCCTTATGAAGGCCAGCTGCTGAAATTAG
*****
AF361746 1514 ATTGGGAGGAGCCTCCACCCACCCCTGACTCCTCCTTATGAAGGCCAGCTGCTGAAATTAG
DNA35639 1561 CTACTCACCAAGAGTGAGGGGCAGAGACTTCCAGTCAGTCAGTGAGTCTCCCAGGCCCTTGA
*****
AF361746 1574 CTACTCACCAAGAGTGAGGGGCAGAGACTTCCAGTCAGTCAGTGAGTCTCCCAGGCCCTTGA
DNA35639 1621 TCTGTACCCCACCCCTATCTAACACCACCCCTGGCTCCACTCCAGCTCCCTGTATTGAT
*****
AF361746 1634 TCTGTACCCCACCCCTATCTAACACCACCCCTGGCTCCACTCCAGCTCCCTGTATTGAT
DNA35639 1681 ATAACCTGTCAGGCTGGTTAGGTTTACTGGGGCAGAGGATAGGAATCTCTTAT
*****
AF361746 1694 ATAACCTGTCAGGCTGGTTAGGTTTACTGGGGCAGAGGATAGGAATCTCTTAT
DNA35639 1741 TAAAACTAACATGAAATATGTGTTGTTTCATTGCAAATTAAATAAGATACTAATG
*****
AF361746 1754 TAAAACTAACATGAAATATGTGTTGTTTCATTGCAAATTAAATAAGATACTAATG
DNA35639 1801 TTTGTATGAAAAA
*****
AF361746 1814 TTTGTATGAAAAA
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>13 P\_AAH02949 Human shear stress-response coding sequence SEQ ID NO: 143. (1827 bp) [1 seg]

Score = 1801 (3570 bits), Expect = 0.0

Identities = 1807/1809 (99%), at 1,13-1809,1821, Strand +/+

DNA35639	1	GGAGCCGCCCTGGGTGTCA	GCGCTCGGCTCCCGCGCACGCTCCGCCGTCGCGCAGCCT
P_AAH02949	13	GGAGCCGCCCTGGGTGTCA	GCGCTCGGCTCCCGCGCACGCTCCGCCGTCGCGCAGCCT
DNA35639	61	CGGCACCTGCAGGTCCGTG	CCTCCCGCGCTGGCGCCCTGACTCCGTCCGCCAGGGA
P_AAH02949	73	CGGCACCTGCAGGTCCGTG	CCTCCCGCGCTGGCGCCCTGACTCCGTCCGCCAGGGA
DNA35639	121	GGGCCATGATTCCCTCCC	GGGGCCCTGGTGA
P_AAH02949	133	GGGCCATGATTCCCTCCC	GGGGCCCTGGTGA
DNA35639	181	GGCTGAGTGCCCTCGCG	CCCCCTCGCGGGCCCAGCTGCAACTGCAC
P_AAH02949	193	GGCTGAGTGCCCTCGCG	CCCCCTCGCGGGCCCAGCTGCAACTGCAC
DNA35639	241	GGTTGCAGGCGGTGGAGG	GAGGGAA
P_AAH02949	253	GGTTGCAGGCGGTGGAGG	GAGGGAA
DNA35639	301	AGGTGTCTTCATCCCAGC	CATGGGAGGTGCC
P_AAH02949	313	AGGTGTCTTCATCCCAGC	CATGGGAGGTGCC
DNA35639	361	AAAAGGAGGATCAGGTG	TGTCC

BLAST RESULTS A-29

P\_AAH02949 373 AAAAGGAGGATCAGGTGTTGCCTACATCAATGGGTACAACAAGCAAACCTGGAGTAT  
DNA35639 421 CCTTGGTCTACTCCATGCCCTCCCGAACCTGTCCTGCGGCTGGAGGGCTCCAGGAGA  
P\_AAH02949 433 CCTTGGTCTACTCCATGCCCTCCCGAACCTGTCCTGCGGCTGGAGGGCTCCAGGAGA  
DNA35639 481 AAGACTCTGGCCCTACAGCTGCTCGTGAATGTGCAAGACAAACAAGGCAAATCTAGGG  
P\_AAH02949 493 AAGACTCTGGCCCTACAGCTGCTCGTGAATGTGCAAGACAAACAAGGCAAATCTAGGG  
DNA35639 541 GCCACAGCATAAAACCTTAGAACTCAATGTAUTGGTCCCTCAGCTCCATCCTGCC  
P\_AAH02949 553 GCCACAGCATAAAACCTTAGAACTCAATGTAUTGGTCCCTCAGCTCCATCCTGCC  
DNA35639 601 GTCTCCAGGGTGTGCCCATGTGGGGCAAACGTGACCTGAGCTGCCAGTCTCCAAGGA  
P\_AAH02949 613 GTCTCCAGGGTGTGCCCATGTGGGGCAAACGTGACCTGAGCTGCCAGTCTCCAAGGA  
DNA35639 661 GTAAGCCGCTGTCCAATACCAGTGGGATCGGCAGCTCCATCCTCCAGACTTCTTG  
P\_AAH02949 673 GTAAGCCTGCTGTCCAATACCAGTGGGATCGGCAGCTCCATCCTCCAGACTTCTTG  
DNA35639 721 CACCAGCATTAGATGTCATCCGTGGTCTTAAGCCTCACCAACCTTCGTCTCCATGG  
P\_AAH02949 733 CACCAGCATTAGATGTCATCCGTGGTCTTAAGCCTCACCAACCTTCGTCTCCATGG  
DNA35639 781 CTGGAGTCTATGTCGAAGGCCACAATGAGGTGGGACTGCCAATGTAATGTGACGC  
P\_AAH02949 793 CTGGAGTCTATGTCGAAGGCCACAATGAGGTGGGACTGCCAATGTAATGTGACGC  
DNA35639 841 TGGAAGTGAGCACAGGCCCTGGAGCTGCAGTGGTCTGGAGCTGTTGTGGTACCTGG  
P\_AAH02949 853 TGGAAGTGAGCACAGGCCCTGGAGCTGCAGTGGTCTGGAGCTGTTGTGGTACCTGG  
DNA35639 901 TTGGACTGGGTTGCTGGCTGGCTGGCCTCTTGTAACCAACGCCGGGCAAGGCCCTGG  
P\_AAH02949 913 TTGGACTGGGTTGCTGGCTGGCCTCTTGTAACCAACGCCGGGCAAGGCCCTGG  
DNA35639 961 AGGAGCCAGCCAATGATATCAAGGAGGATGCCATTGCTCCCCGGACCTGCCCTGGCCCA  
P\_AAH02949 973 AGGAGCCAGCCAATGATATCAAGGAGGATGCCATTGCTCCCCGGACCTGCCCTGGCCCA  
DNA35639 1021 AGAGCTCAGACACAATCTCAAGAATGGGACCCCTTCCTCTGTCACCTCCGACGAGCCC  
P\_AAH02949 1033 AGAGCTCAGACACAATCTCAAGAATGGGACCCCTTCCTCTGTCACCTCCGACGAGCCC  
DNA35639 1081 TCCGGCCACCCATGGCCCTCCAGGCCTGGTGCATTGACCCCCACGCCAGTCTCTCCA  
P\_AAH02949 1093 TCTGGCCACCCATGGCCCTCCAGGCCTGGTGCATTGACCCCCACGCCAGTCTCTCCA  
DNA35639 1141 GCCAGGCCCTGCCCTACCAAGACTGCCACGACAGATGGGCCCACCTCAACCAATAT  
P\_AAH02949 1153 GCCAGGCCCTGCCCTACCAAGACTGCCACGACAGATGGGCCCACCTCAACCAATAT  
DNA35639 1201 CCCCCATCCCTGGTGGGTTCTTCCTCTGGCTTGAGCCGATGGTGCTGCCTGTGA

BLAST RESULTS A-30

P\_AAH02949 1213 CCCCCATCCCTGGTGGGGTTCTTCCTCTGGCTTGAGCCGCATGGGTGCTGTGCCTGTGA  
DNA35639 1261 TGGTGCCTGCCAGAGTCAGCTGGCTCTGGTATGATGACCCCACCACTCATTGGCTA  
\*\*\*\*\*  
P\_AAH02949 1273 TGGTGCCTGCCAGAGTCAGCTGGCTCTGGTATGATGACCCCACCACTCATTGGCTA  
DNA35639 1321 AAGGATTGGGGTCTCTCCTCTATAAGGGTCACCTCTAGCACAGAGGCCTGAGTCATG  
\*\*\*\*\*  
P\_AAH02949 1333 AAGGATTGGGGTCTCTCCTCTATAAGGGTCACCTCTAGCACAGAGGCCTGAGTCATG  
DNA35639 1381 GGAAAGAGTCACACTCCTGACCCTTAGTACTCTGCCCCACCTCTTTACTGTGGAAA  
\*\*\*\*\*  
P\_AAH02949 1393 GGAAAGAGTCACACTCCTGACCCTTAGTACTCTGCCCCACCTCTTTACTGTGGAAA  
DNA35639 1441 ACCATCTCAGTAAGACCTAACAGTGTCCAGGAGACAGAAGGAGAAGAGGAAGTGGATCTGGA  
\*\*\*\*\*  
P\_AAH02949 1453 ACCATCTCAGTAAGACCTAACAGTGTCCAGGAGACAGAAGGAGAAGAGGAAGTGGATCTGGA  
DNA35639 1501 ATTGGGAGGAGCCTCCACCCACCCCTGACTCCTTATGAAGCCAGCTGCTGAAATTAG  
\*\*\*\*\*  
P\_AAH02949 1513 ATTGGGAGGAGCCTCCACCCACCCCTGACTCCTTATGAAGCCAGCTGCTGAAATTAG  
DNA35639 1561 CTACTCACCAAGAGTGAGGGGCAGAGACTTCCAGTCAGTCACTGAGTCTCCAGGCCCTTGA  
\*\*\*\*\*  
P\_AAH02949 1573 CTACTCACCAAGAGTGAGGGGCAGAGACTTCCAGTCAGTCACTGAGTCTCCAGGCCCTTGA  
DNA35639 1621 TCTGTACCCACCCCTATCTAACACCACCCCTGGCTCCACTCCAGCTCCCTGTATTGAT  
\*\*\*\*\*  
P\_AAH02949 1633 TCTGTACCCACCCCTATCTAACACCACCCCTGGCTCCACTCCAGCTCCCTGTATTGAT  
DNA35639 1681 ATAACCTGTCAGGCTGGTTAGGTTACTGGGGCAGAGGATAGGAATCTTTAT  
\*\*\*\*\*  
P\_AAH02949 1693 ATAACCTGTCAGGCTGGTTAGGTTACTGGGGCAGAGGATAGGAATCTTTAT  
DNA35639 1741 TAAAACTAACATGAAATATGTGTTGTTTCATTGCAAATTAAATAAGATAACATAATG  
\*\*\*\*\*  
P\_AAH02949 1753 TAAAACTAACATGAAATATGTGTTGTTTCATTGCAAATTAAATAAGATAACATAATG  
DNA35639 1801 TTTGTATGA  
\*\*\*\*\*  
P\_AAH02949 1813 TTTGTATGA

>14 P\_AAZ65278 Human secreted protein gene 29. (1932 bp) [1 seg]  
Score = 1785 (3539 bits), Expect = 0.0  
Identities = 1804/1810 (99%), Gaps = 2/1810 (0%), at 4,9-1813,1816, Strand +/-

DNA35639 4 GCGGCCCTGGGTGTCAGCGGCTCGGCTCCCGCGCACGCTCCGGCGTCGCGCAGCCTCGG  
\*\*\*\*\*  
P\_AAZ65278 9 GCGGCCCTGGGTGTCAGCGGCTCGGCTCCCGCGCACGCTCCGGCGTCGCGCA-SCTCGG  
DNA35639 64 CACCTGCAGGTCCGTGCGTCCCGCGCTGGCGCCCTGACTCCGTCCGGCCAGGGAGGG  
\*\*\*\*\*  
P\_AAZ65278 68 CACCTGCAGGTCCGTGCGTCCCGCGCTGGCGCCCTGACTCCGTCCGGCCAGGGAGGG  
DNA35639 124 CCATGATTCCCTCCGGGCCCCCTGGTACCAACTTGCTGCGGTTTTGTTCCCTGGGC  
\*\*\*\*\*  
P\_AAZ65278 128 CCATGATTCCCTCCGGGCCCCCTGGTACCAACTTGCTGCGGTTTTGTTCCCTGGGC

DNA35639	184	TGAGTGCCTCGCCCCCCTCGCGGGCCAGCTGCAACTGCACTTGCCGCCAACCGGT *****
P_AAZ65278	188	TGAGTGCCTCGCCCCCCTCGCGGGCCAGCTGCAACTGCACTTGCCGCCAACCGGT *****
DNA35639	244	TGCAGGCGGTGGAGGGAGGGGAAGTGGTCTTCAGCGTGGTACACCTGCACGGGGAGG *****
P_AAZ65278	248	TGCAGGCGGTGGAGGGAGGGGAAGTGGTCTTCAGCGTGGTACANTTGCACGGGGAGG *****
DNA35639	304	TGTCTTCATCCCAGCCATGGGAGGTGCCCTTGTGATGTGGTTCTTCAAACAGAAAGAAA *****
P_AAZ65278	308	TGTCTTCATCCCAGCCATGGGAGGTGCCCTTGTGATGTGGTTCTTCAAACAGAAAGAAA *****
DNA35639	364	AGGAGGATCAGGTGTTGCTCACATCAATGGGGTACAACAAGCAAACCTGGAGTATCCT *****
P_AAZ65278	368	AGGAGGATCAGGTGTTGCTCACATCAATGGGGTACAACAAGCAAACCTGGAGTATCCT *****
DNA35639	424	TGGTCTACTCCATGCCCTCCCGAACCTGTCCTGCGGCTGGAGGGTCTCCAGGAGAAAG *****
P_AAZ65278	428	TGGTCTACTCCATGCCCTCCCGAACCTGTCCTGCGGCTGGAGGGTCTCCAGGAGAAAG *****
DNA35639	484	ACTCTGGCCCCTACAGCTGCTCCGTGAATGTGCAAGACAAACAAGGCAAATCTAGGGCC *****
P_AAZ65278	488	ACTCTGGCCCCTACAGCTGCTCCGTGAATGTGCAAGACAAACAAGGCAAATCTAGGGCC *****
DNA35639	544	ACAGCATAAAACCTTAGAACTCAATGTACTGGTTCTCCAGCTCCTCCATCCTGCCGTC *****
P_AAZ65278	548	ACAGCATAAAACCTTAGAACTCAATGTACTGGTTCTCCAGCTCCTCCATCCTGCCGTC *****
DNA35639	604	TCCAGGGTGTGCCCATGTGGGGCAAACGTGACCTGAGCTGCCAGTCTCCAAGGAGTA *****
P_AAZ65278	608	TCCAGGGTGTGCCCATGTGGGGCAAACGTGACCTGAGCTGCCAGTCTCCAAGGAGTA *****
DNA35639	664	AGCCCGCTGTCCAATACCAGTGGGATCGCAGCTCCATCCTCCAGACTTCTTCAC *****
P_AAZ65278	668	AGCCCGCTGTCCAATACCAGTGGGATCGCAGCTCCATCCTCCAGACTTCTTCAC *****
DNA35639	724	CAGCATTAGATGTCATCCGTGGTCTTAAGCCTCACCAACCTTCGTCTCCATGGCTG *****
P_AAZ65278	728	CAGCATTAGATGTCATCCGTGGTCTTAAAGCCTCACCAACCTTCGTCTCCATGGCTG *****
DNA35639	784	GAGTCTATGTCTGCAAGGCCACAATGAGGTGGGACTGCCAATGTAATGTGACGCTGG *****
P_AAZ65278	788	GAGTCTATGTCTGCAAGGCCACAATGAGGTGGGACTG-CCAATGTAATGTGACGCTGG *****
DNA35639	844	AAGTGAGCACAGGGCTGGAGCTGCAGTGGTGTGGAGCTGTTGTGGGTACCTGGTTG *****
P_AAZ65278	847	AAGTGAGCACAGGGCTGGAGCTGCAGTGGTGTGGAGCTGTTGTGGGTACCTGGTTG *****
DNA35639	904	GACTGGGTTGCTGGCTGGCTGGCCTTGTACCAACGCCGGGGCAAGGCCCTGGAGG *****
P_AAZ65278	907	GACTGGGTTGCTGGCTGGCCTTGTACCAACGCCGGGGCAAGGCCCTGGAGG *****
DNA35639	964	AGCCAGCCAATGATATCAAGGAGGATGCCATTGCTCCCCGGACCCCTGCCCTGGCCAAGA *****
P_AAZ65278	967	AGCCAGCCAATGATATCAAGGAGGATGCCATTGCTCCCCGGACCCCTGCCCTGGCCAAGA *****

BLAST RESULTS A-32

DNA35639	1024	GCTCAGACACAATCTCAAGAATGGGACCCTTCCTCTGTCACCTCCGCACGCCCTCC *****
P_AAZ65278	1027	GCTCAGACACAATCTCAAGAATGGGACCCTTCCTCTGTCACCTCCGCACGCCCTCC *****
DNA35639	1084	GGCCACCCATGGCCCTCCCAGGCCTGGTCATTGACCCCCACGCCAGTCTCTCCAGCC *****
P_AAZ65278	1087	GGCCACCCATGGCCCTCCCAGGCCTGGTCATTGACCCCCACGCCAGTCTCTCCAGCC *****
DNA35639	1144	AGGCCCTGCCCTACCAAGACTGCCACGACAGATGGGCCACCCCTAACCAATACTCC *****
P_AAZ65278	1147	AGGCCCTGCCCTACCAAGACTGCCACGACAGATGGGCCACCCCTAACCAATACTCC *****
DNA35639	1204	CCATCCCTGGTGGGTTCTCCTCTGGCTTGAGCCGCATGGTGTGCGCTGTGATGG *****
P_AAZ65278	1207	CCATCCCTGGTGGGTTCTCCTCTGGCTTGAGCCGCATGGTGTGCGCTGTGATGG *****
DNA35639	1264	TGCCTGCCAGAGTCAGCTGGCTCTGGTATGATGACCCCACCACTCATGGCTAAAG *****
P_AAZ65278	1267	TGCCTGCCAGAGTCAGCTGGCTCTGGTATGATGACCCCACCACTCATGGCTAAAG *****
DNA35639	1324	GATTTGGGTCTCTCCTTCTATAAGGGTCACCTCTAGCACAGAGGCCCTGAGTCATGGGA *****
P_AAZ65278	1327	GATTTGGGTCTCTCCTTCTATAAGGGTCACCTCTAGCACAGAGGCCCTGAGTCATGGGA *****
DNA35639	1384	AAGAGTCACACTCCTGACCCCTAGTACTCTGCCACCTCTTTACTGTGGAAAACC *****
P_AAZ65278	1387	AAGAGTCACACTCCTGACCCCTAGTACTCTGCCACCTCTTTACTGTGGAAAACC *****
DNA35639	1444	ATCTCAGTAAGACCTAAGTGTCCAGGAGACAGAAGGAGAAGAGGAAGTGGATCTGGAATT *****
P_AAZ65278	1447	ATCTCAGTAAGACCTAAGTGTCCAGGAGACAGAAGGAGAAGAGGAAGTGGATCTGGAATT *****
DNA35639	1504	GGGAGGAGCCTCCACCCACCCCTGACTCCTCTTATGAAGGCCAGCTGCTGAAATTAGCTA *****
P_AAZ65278	1507	GGGAGGAGCCTCCACCCACCCCTGACTCCTCTTATGAAGGCCAGCTGCTGAAATTAGCTA *****
DNA35639	1564	CTCACCAAGAGTGAGGGCAGAGACTTCCAGTCACTGAGTCTCCAGGCCCTTGATCT *****
P_AAZ65278	1567	CTCACCAAGAGTGAGGGCAGAGACTTCCAGTCACTGAGTCTCCAGGCCCTTGATCT *****
DNA35639	1624	GTACCCCACCCCTATCTAACACCACCCCTGGCTCCACTCCAGCTCCCTGTATTGATATA *****
P_AAZ65278	1627	GTACCCCACCCCTATCTAACACCACCCCTGGCTCCACTCCAGCTCCCTGTATTGATATA *****
DNA35639	1684	ACCTGTCAGGCTGGTTGGTAGGTTACTGGGCAGAGGATAGGAAATCTCTTATTAA *****
P_AAZ65278	1687	ACCTGTCAGGCTGGTTGGTAGGTTACTGGGCAGAGGATAGGAAATCTCTTATTAA *****
DNA35639	1744	AACTAACATGAAATATGTGTTTTCATTGCAAATTAAATAAGATAACATAATGTTT *****
P_AAZ65278	1747	AACTAACATGAAATATGTGTTTTCATTGCAAATTAAATAAGATAACATAATGTTT *****
DNA35639	1804	GTATGAAAAA *****
P_AAZ65278	1807	GTATGARAAA

>15 P\_AAF45017 Human secreted protein related coding sequence SEQ ID NO: 141.  
 (1869 bp) [1 seg]  
 Score = 1731 (3431 bits), Expect = 0.0  
 Identities = 1795/1812 (99%), Gaps = 4/1812 (0%), at 1,28-1809,1838, Strand +/+

DNA35639	1	GGAGCCGCCCTGGGTGTCAGCGCTCGGCTCCCGCGCACGCTCCGGCGTCGCAGCCT
		*****
P_AAF45017	28	GGAGCCGCCCTGGGTGTCAGCGCTCGGCTCCCGCGCACGCTCCGGCGTCGCAGCCT
		*****
DNA35639	61	CGGCACCTGCAGGTCCGTGCGTCCC CGCGCTGGCGCCCGTACTCCGTCCGGCCAGGGA
		*****
P_AAF45017	88	CGGCACCTGCAGGTCCGTGCGTCCC CGCGCTGGCGCCCGTACTCCGTCCGGCCAGGGA
		*****
DNA35639	121	GGGCCATGATTCCCTCCCGGGGCCCTGGTGACCAACTTGCTGCGGTTTTGTTCCCTGG
		*****
P_AAF45017	148	GGGCCATGATTCCCTCCCGGGGCCCTGGTGACCAACTTGNTGCGGTTTTGTTCCCTGG
		*****
DNA35639	181	GGCTGAGTGCCTCGCGCCCCCTCGCGGGCCAGCTGCAACTGCACTTGCCGCCAAC
		*****
P_AAF45017	208	GGCTGAGTGCCTCGCGCCCCCTCGCGGGCCAGCTGCAACTGCACTTGCCGCCAAC
		*****
DNA35639	241	GGTGCAGGCGGTGGAGG-GAGGGGAAGTGGTGCTTCCAGCGTGGTACACCTTGACCGG
		*****
P_AAF45017	268	GGTGCAGGCGGTGGAGGAGGGGAAAGTGGTGCTT-CAGCATGGTACACCTTGACAGG
		*****
DNA35639	300	GAGGTGTTCTCATCCCAGCCATGGGAGGTGCCCTTGTGATGTGGTTCTCAAACAGAAA
		*****
P_AAF45017	327	GAGGTGTTCTCATCCCAGCCATGGGAGGTGCCCTTGTGATGTGGTTCTCAAACAGAAA
		*****
DNA35639	360	GAAAAGGAGGATCAGGTGTTGCTACATCAATGGGTACAACAAGCAAACCTGGAGTA
		*****
P_AAF45017	387	GAAAAGGAGGATCAGGTGTTGCTACATCAATGGGTACAACAAGCAAACCTGGAGTA
		*****
DNA35639	420	TCCTGGTCTACTCCATGCCCTCCCGAACCTGCTCCCTGCGGCTGGAGGGTCTCCAGGAG
		*****
P_AAF45017	447	TCCTGGTCTACTCCATGCCCTCCCGAACCTGCTCCCTGCGGCTGGAGGGTCTCCAGGAG
		*****
DNA35639	480	AAAGACTCTGGCCCTACAGCTGCTCCGTGAATGTGCAAGACAACAAGCAAATCTAGG
		*****
P_AAF45017	507	AAAGACTCTGGCCCTACAGCTGCTCCGTGAATGTGCAAGACAACAAGCAAATCTAGG
		*****
DNA35639	540	GGCACAGCATAAAACCTTAGAACTCAATGTACTGGTCCTCCAGCTCCATCCTGC
		*****
P_AAF45017	567	GGCACAGCATAAAACCTTAGAACTCAATGTACTGGTCCTCCAGCTCCATCCTGC
		*****
DNA35639	600	CGTCTCCAGGGTGTGCCCATGTGGGGCAACGTGACCTGAGCTGCCAGTCTCCAAGG
		*****
P_AAF45017	627	CGTCTCCAGGGTGTGCCCATGTGGGGCAACGTGACCTGAGCTGCCAGTCTCCAAGG
		*****
DNA35639	660	AGTAAGCCCGCTGCTCAATACCAGTGGGATCGGCAGCTTCCATCCTCCAGACTTTCTTT
		*****
P_AAF45017	687	AGTAAGCCGTTGCTCAATACCAGTGGGATCGGCAGCTTCCATCCTCCAGACTTTCTTT
		*****
DNA35639	720	GCACCAGCATTAGATGTCATCCGTGGGTCTTAAGCCTCACCAACCTTCTGCATG
		*****
P_AAF45017	747	GCACCAGCATTAGATGTCATCCGTGGGTCTTAAGCCTCACCAACCTTCTGCATG

BLAST RESULTS A-3A

DNA35639	780	GCTGGAGTCTATGTCTGCAAGGCCACAATGAGGTGGCACTGCCAATGTAATGTGACG *****
P_AAF45017	807	GCTGGAGTCTATGTCTGCAAGGCCACAATGAGGTGGCACTGCCAATGTAATGTGACG *****
DNA35639	840	CTGGAAGTGAGCACAGGCCCTGGAGCTGCAGTGGTGCTGGAGCTGTTGGTACCCCTG *****
P_AAF45017	867	CTGGAAGTGAGCACAGGCCCTGGAGCTGCAGTGGTGCTGAAGCTGTTGGTACCCCTG *****
DNA35639	900	GTTGGACTGGGTTGCTGGCTGGCTGGCCTTGTACCAACGCCGGGCAAGGCCCTG *****
P_AAF45017	927	GTTGGACTGGGTTGCTGGCTGGCCTTGTACCAACGCCGGGCAAGGCCCTG *****
DNA35639	960	GAGGAGCCAGCCAATGATATCAAGGAGGATGCCATTGCTCCCCGGACCCCTGCCCTGGCCC *****
P_AAF45017	987	GAGGAGCCAGCCAATGATATCAAGGAGGATGCCATTGCTCCCCGGACCCCTGCCCTGGCCC *****
DNA35639	1020	AAGAGCTCAGACACAATCTCCAAGAACATGGGACCCCTTCCTCTGTCACCTCCGACAGGCC *****
P_AAF45017	1047	AAGAGCTCAGACACAATCTCCAAGAACATGGGACCCCTTCCTCTGTCACCTCCGACAGGCC *****
DNA35639	1080	CTCCGGCCACCCCATGGCCCTCCCAGGCCTGGTGCAATTGACCCCCACGCCAGTCTCTCC *****
P_AAF45017	1107	CTCCGGCCACCCCATGGCCCTCCCAGGCCTGGTGCAATTGACCCCCACGCCAGTCTATCC *****
DNA35639	1140	AGCCAGGCCCTGCCCTACCAAGAC-TGCCACGACAGATGGGGCCACCCCTAACCAAT *****
P_AAF45017	1167	AGCCAGGCCCTGCCCTACCAAGACATGCCACGACAGATGGGGCCACCCCTAACCAAT *****
DNA35639	1199	ATCCCCCATCCCTGGTGGGTTCTTCCTCTGGC-TTGAGCCGATGGTGCTGTGCCTG *****
P_AAF45017	1227	ATCCCCCATCCCTGGTGGGTTTTTCCTTGGCTTGAGCCGATGGTGCTGNCCCTG *****
DNA35639	1258	TGATGGTGCCTGCCAGAGTCAGCTGGCTCTGGTATGATGACCCCACCACTCATTGG *****
P_AAF45017	1287	TGATGGNGCCTGCCAGAGTCAGCTGGCTCTGGTATGATGACCCCACCACTCATTGG *****
DNA35639	1318	CTAAAGGATTGGGTCTCTCCTTATAAGGTCACCTCTAGCACAGAGGCCTGAGTC *****
P_AAF45017	1347	CTAAAGGATTGGGTCTCTCCTTATAAGGTCACCTCTAGCACAGAGGCCTGAGTC *****
DNA35639	1378	ATGGGAAAGAGTCACACTCCTGACCCTTAGTACTCTGCCACCTCTTTACTGTGGG *****
P_AAF45017	1407	ATGGGAAAGAGTCACACTCCTGACCCTTAGTACTCTGCCACCTCTTTACTGTGGG *****
DNA35639	1438	AAAACCATCTCAGTAAGACCTAAGTGTCCAGGAGACAGAAGGAGAACAGAAGTGGATCT *****
P_AAF45017	1467	AAAACCATCTCAGTAAGACCTAAGTGTCCAGGAGACAGAAGGAGAACAGAAGTGGATCT *****
DNA35639	1498	GGAATTGGGAGGAGCCTCACCCACCCCTGACTCCTCCTTATGAAGCCAGCTGCTGAAAT *****
P_AAF45017	1527	GGAATTGGGAGGAGCCTCACCCACCCCTGACTCCTCCTTATGAAGCCAGCTGCTGAAAT *****
DNA35639	1558	TAGCTACTCACCAAGAGTGAGGGCAGAGACTTCCAGTCAGTGAGTCTCCAGGCCCT *****
P_AAF45017	1587	TAGCTACTCACCAAGAGTGAGGGCAGAGACTTCCAGTCAGTGAGTCTCCAGGCCCT *****
DNA35639	1618	TGATCTGTACCCACCCCTATCTAACACCACCCCTGGCTCCACTCCAGCTCCGTATT *****

\*\*\*\*\*  
P\_AAF45017 1647 TGATCTGTACCCCACCCCTATCTAACACCACCTGGCTCCACTCCAGCTCCCTGTATT  
DNA35639 1678 GATATAACCTGTCAGGCTGGCTGGTTAGGTTTACTGGGCAGAGGATAGGAATCTCT  
\*\*\*\*\*  
P\_AAF45017 1707 GATATAACCTGTCAGGCTGGCTGGTTAGGTTTACTGGGCAGAGGATAGGAATCTCT  
DNA35639 1738 TATTAAAACTAACATGAAATATGTGTTTTCAATTGCAAATTAAATAAAGATACATA  
\*\*\*\*\*  
P\_AAF45017 1767 TATTAAAACTAACATGAAATATGTGTTTTCAATTGCAAATTAAATAAAGATACATA  
DNA35639 1798 ATGTTGTATGA  
\*\*\*\*\*  
P\_AAF45017 1827 ATGTTGTATGA

>16 P\_AAF45016 Human secreted protein related coding sequence SEQ ID NO: 139.  
(1869 bp) [1 seg]  
Score = 1731 (3431 bits), Expect = 0.0  
Identities = 1795/1812 (99%), Gaps = 4/1812 (0%), at 1,28-1809,1838, Strand +/-

DNA35639 1 GGAGCCGCCCTGGGTGTCAGGGCTCGGCTCCCGCGCACGCTCCGGCCGTCGCGCAGCCT  
\*\*\*\*\*  
P\_AAF45016 28 GGAGCCGCCCTGGGTGTCAGGGCTCGGCTCCCGCGCACGCTCCGGCCGTCGCGCAGCCT  
DNA35639 61 CGGCACCTGCAGGTCCGTGCGTCCCGCGCTGGCGCCCTGACTCCGTCCGGCCAGGGA  
\*\*\*\*\*  
P\_AAF45016 88 CGGCACCTGCAGGTCCGTGCGTCCCGCGCTGGCGCCCTGACTCCGTCCGGCCAGGGA  
DNA35639 121 GGGCCATGATTCCCTCCGGGCCCTGGTGACCAACTTGCTGCGGTTTTGTTCTGG  
\*\*\*\*\*  
P\_AAF45016 148 GGGCCATGATTCCCTCCGGGCCCTGGTGACCAACTGNTGCGGTTTTGTTCTGG  
DNA35639 181 GGCTGAGTGCCCTCGCGCCCCCTCGCGGGCCAGCTGCAACTGCACTTGCCCCGCCAAC  
\*\*\*\*\*  
P\_AAF45016 208 GGCTGAGTGCCCTCGCGCCCCCTCGCGGGCCAGCTGCAACTGCACTTGCCCCGCCAAC  
DNA35639 241 GGTTGCAGGCGGTGGAGG-GAGGGGAAGTGGTGCTTCCAGCGTGGTACACCTGCACGGG  
\*\*\*\*\*  
P\_AAF45016 268 GGTTGCAGGCAGGTGGAGGAGGGGAAAGTGGTGCTT-CAGCATGGTACACCTGACAGG  
DNA35639 300 GAGGTGTCTTCATCCCAGCCATGGGAGGTGCCCTTGTGATGTGGTTCTCAAACAGAAA  
\*\*\*\*\*  
P\_AAF45016 327 GAGGTGTCTTCATCCCAGCCATGGGAGGTGCCCTTGTGATGTGGTTCTCAAACAGAAA  
DNA35639 360 GAAAAGGAGGATCAGGTGTTGCTACATCAATGGGTACAACAAGCAAACCTGGAGTA  
\*\*\*\*\*  
P\_AAF45016 387 GAAAAGGAGGATCAGGTGTTGCTACATCAATGGGTACAACAAGCAAACCTGGAGTA  
DNA35639 420 TCCTTGGTCTACTCCATGCCCTCCCGAACCTGTCCTGCGGCTGGAGGGTCTCCAGGAG  
\*\*\*\*\*  
P\_AAF45016 447 TCCTTGGTCTACTCCATGCCCTCCCGAACCTGTCCTGCGGCTGGAGGGTCTCCAGGAG  
DNA35639 480 AAAGACTCTGGCCCTACAGCTGCTCCGTGAATGTGCAAGACAAACAAGGCAAATCTAGG  
\*\*\*\*\*  
P\_AAF45016 507 AAAGACTCTGGCCCTACAGCTGCTCCGTGAATGTGCAAGACAAACAAGGCAAATCTAGG  
DNA35639 540 GGCCACAGCATAAAACCTTAGAACTCAATGTACTGGTCTCCAGCTCCTCATCCTGC

BLAST RESULTS A-B39

P_AAF45016	567	***** GGCCACAGCATAAAACCTTAGAACTCAATGTACTGGTCCCTCAGCTCCATCTGC
DNA35639	600	CGTCTCCAGGGTGTCCCCATGTGGGGCAAACGTGACCTGAGCTGCCAGTCTCCAAGG *****
P_AAF45016	627	CGTATCCAGGGTGTCCCCATGTGGGGCAAACGTGACCTGAGCTGCCAGTCTCCAAGG *****
DNA35639	660	AGTAAGCCCCTGTCCAATACCAGTGGGATCGGCAGCTTCATCCTCCAGACTTTCTTT *****
P_AAF45016	687	AGTAAGCCCCTGTCCAATACCAGTGGGATCGGCAGCTTCATCCTCCAGACTTTCTTT *****
DNA35639	720	GCACCAGCATTAGATGTCATCCGTGGTCTTAAGCCTCACCAACCTTCGTCTTCATG *****
P_AAF45016	747	GCACCAGCATTAGATGTCATCCGTGGTCTTAAGCCTCACCAACCTTCGTCTTCATG *****
DNA35639	780	GCTGGAGTCTATGTCAGGCCCACAATGAGGTGGCACTGCCAATGTAATGTGACG *****
P_AAF45016	807	GCTGGAGTCTATGTCAGGCCCACAATGAGGTGGCACTGCCAATGTAATGTGACG *****
DNA35639	840	CTGGAAGTGAGCACAGGGCTGGAGCTGCAGTGGTGCTGGAGCTGTTGGTACCCCTG *****
P_AAF45016	867	CTGGAAGTGAGCACAGGGCTGGAGCTGCAGTGGTGCTGAAGCTGTTGGTACCCCTG *****
DNA35639	900	GTTGGACTGGGTTGCTGGCTGGCTGGCCTTGTACCAACGCCGGGCAAGGCCCTG *****
P_AAF45016	927	GTTGGACTGGGTTGCTGGCTGGCCTTGTACCAACGCCGGGCAAGGCCCTG *****
DNA35639	960	GAGGAGCCAGCCAATGATATCAAGGAGGATGCCATTGCTCCCCGACCTGCCCTGGCC *****
P_AAF45016	987	GAGGAGCCAGCCAATGATATCAAGGAGGATGCCATTGCTCCCCGACCTGCCCTGGCC *****
DNA35639	1020	AAGAGCTCAGACACAATCTCCAAGAACATGGGACCCCTTCCTCTGTCACCTCCGCACGAGCC *****
P_AAF45016	1047	AAGAGCTCAGACACAATCTCCAAGAACATGGGACCCCTTCCTCTGTCACCTCCGCACGAGCC *****
DNA35639	1080	CTCCGGCCACCCCATGGCCCTCCCAGGCCTGGTGCAATTGACCCCCACGCCAGTCTCTCC *****
P_AAF45016	1107	CTCCGGCCACCCCATGGCCCTCCCAGGCCTGGTGCAATTGACCCCCACGCCAGTCTATCC *****
DNA35639	1140	AGCCAGGCCCTGCCCTACCAAGAC-TGCCACGACAGATGGGCCACCCCTAACCAAT *****
P_AAF45016	1167	AGCCAGGCCCTGCCCTACCAAGACATGCCACGACAGATGGGCCACCCCTAACCAAT *****
DNA35639	1199	ATCCCCCATCCCTGGTGGGTTCTCCTCTGGC-TTGAGCCGCATGGTGCTGTGCCTG *****
P_AAF45016	1227	ATCCCCCATCCCTGGTGGGTTCTCCTCTGGCATTGAGCCGCATGGTGCTGNCCCTG *****
DNA35639	1258	TGATGGTGCCTGCCAGAGTCAGACTGGCTCTGGTATGATGACCCCCACCAACTCATTGG *****
P_AAF45016	1287	TGATGGNGCCTGCCAGAGTCAGACTGGCTCTGGTATGATGACCCCCACCAACTCATTGG *****
DNA35639	1318	CTAAAGGATTGGGTCTCCTTCTATAAGGTACACCTCTAGCACAGAGGCCTGAGTC *****
P_AAF45016	1347	CTAAAGGATTGGGTCTCCTTCTATAAGGTACACCTCTAGCACAGAGGCCTGAGTC *****
DNA35639	1378	ATGGGAAAGAGTCACACTCCTGACCTTAGTACTCTGCCACCTCTTTACTGTGGG *****

BLAST RESULTS A-37

P\_AAF45016 1407 ATGGGAAAGAGTCACACTCCTGACCCTAGTACTCTGCCAACCTCTTTACTGTGGG  
DNA35639 1438 AAAACCATCTCAGTAAGACCTAAGTGTCCAGGAGACAGAAGGAGAAGAGGAAGTGGATCT  
\*\*\*\*\*  
P\_AAF45016 1467 AAAACCATCTCAGTAAGACCTAAGTGTCCAGGAGACAGAAGGAGAAGAGGAAGTGGATCT  
DNA35639 1498 GGAATTGGGAGGAGCCTCCACCCACCCCTGACTCCTCCTTATGAAGCCAGCTGCTGAAAT  
\*\*\*\*\*  
P\_AAF45016 1527 GGAATTGGGAGGAGCCTCCACCCACCCCTGACTCCTCCTTATGAAGCCAGCTGCTGAAAT  
DNA35639 1558 TAGCTACTCACCAAGAGTGAGGGGCAGAGACTTCCAGTCAGTGAGTCTCCCAGGCCCT  
\*\*\*\*\*  
P\_AAF45016 1587 TAGCTACTCACCAAGAGTGAGGGGCAGAGACTTCCAGTCAGTGAGTCTCCCAGGCCCT  
DNA35639 1618 TGATCTGTACCCACCCCTATCTAACACCACCCCTGGCTCCACTCCAGCTCCCTGTATT  
\*\*\*\*\*  
P\_AAF45016 1647 TGATCTGTACCCACCCCTATCTAACACCACCCCTGGCTCCACTCCAGCTCCCTGTATT  
DNA35639 1678 GATATAACCTGTCAGGCTGGCTGGTTAGGTTTACTGGGGCAGAGGATAGGAATCTCT  
\*\*\*\*\*  
P\_AAF45016 1707 GATATAACCTGTCAGGCTGGCTGGTTAGGTTTACTGGGGCAGAGGATAGGAATCTCT  
DNA35639 1738 TATTAAAACTAACATGAAATATGTGTTTTCATTTGCAAATTAAATAAGATAACATA  
\*\*\*\*\*  
P\_AAF45016 1767 TATTAAAACTAACATGAAATATGTGTTTTCATTTGCAAATTAAATAAGATAACATA  
DNA35639 1798 ATGTTTGATGA  
\*\*\*\*\*  
P\_AAF45016 1827 ATGTTTGATGA

>17 P\_AAF45014 Human secreted protein related coding sequence SEQ ID NO: 135.  
(1869 bp) [1 seg]  
Score = 1731 (3431 bits), Expect = 0.0  
Identities = 1795/1812 (99%), Gaps = 4/1812 (0%), at 1,28-1809,1838, Strand +/-

DNA35639 1 GGAGCCGCCCTGGGTGTCAGCGCTCGGCTCCGCGCACGCTCCGGCGTCGCGCAGCCT  
\*\*\*\*\*  
P\_AAF45014 28 GGAGCCGCCCTGGGTGTCAGCGCTCGGCTCCGCGCACGCTCCGGCGTCGCGCAGCCT  
DNA35639 61 CGGCACCTGCAGGTCGTGCGTCCCGCGCTGGCGCCCTGACTCCGTCCGGCCAGGGA  
\*\*\*\*\*  
P\_AAF45014 88 CGGCACCTGCAGGTCGTGCGTCCCGCGCTGGCGCCCTGACTCCGTCCGGCCAGGGA  
DNA35639 121 GGGCCATGATTCCTCCCTCCGGGCCCTGGTGACCAACTTGCTGCGGTTTGTCTGG  
\*\*\*\*\*  
P\_AAF45014 148 GGGCCATGATTCCTCCCTCCGGGCCCTGGTGACCAACTTGNTGCGGTTTGTCTGG  
DNA35639 181 GGCTGAGTGCCTCGCGCCCCCTCGCGGGCCAGCTGCAACTGCACTTGCCC GCCAACCC  
\*\*\*\*\*  
P\_AAF45014 208 GGCTGAGTGCCTCGCGCCCCCTCGCGGGCCAGCTGCAACTGCACTTGCCC GCCAACCC  
DNA35639 241 GGTTGCAGGC GG TGAGG-GAGGGGAAGTGGTGCTTCCAGCGTGGTACACCTGCACGGG  
\*\*\*\*\*  
P\_AAF45014 268 GGTTGCAGGC GG TGAGGAGGGGAAAGTGGTGCTT-CAGCATGGTACACCTGCACAGG  
DNA35639 300 GAGGTGTCTTCATCCCAGCCATGGGAGGTGCCCTTGTGATGTGGTTCTCAAACAGAAA  
\*\*\*\*\*

BEST RESULTS A-30

P_AAF45014	327	GAGGCCTTCCATCCCAGCCATGGGAGGTGCCCTTGTGATGTGGTTCTCAAACAGAAA
DNA35639	360	GAAAAGGAGGATCAGGTGTTGCTTACATCAATGGGTACAACAAGCAAACCTGGAGTA *****
P_AAF45014	387	GAAAAGGAGGATCAGGTGTTGCTTACATCAATGGGTACAACAAGCAAACCTGGAGTA
DNA35639	420	TCCTTGGTCTACTCCATGCCCTCCCGAACCTGTCCTGCCGTGGAGGTCTCCAGGAG *****
P_AAF45014	447	TCCTTGGTCTACTCCATGCCCTCCCGAACCTGTCCTGCCGTGGAGGTCTCCAGGAG
DNA35639	480	AAAGACTCTGGCCCTACAGCTGCTCCGTGAATGTCAAGACAAACAAGGCAAATCTAGG *****
P_AAF45014	507	AAAGACTCTGGCCCTACAGCTGCTCCGTGAATGTCAAGACAAACAAGGCAAATCTAGG
DNA35639	540	GGCCACAGCATAAAACCTTAGAACTCAATGTACTGGTCCTCCAGCTCCTCCATCCTGC *****
P_AAF45014	567	GGCCACAGCATAAAACCTTAGAACTCAATGTACTGGTCCTCCAGCTCCTCCATCCTGC
DNA35639	600	CGTCTCCAGGTGTGCCCATGTGGGGCAAACGTGACCCTGAGCTGCCAGTCTCCAAGG *****
P_AAF45014	627	CGTCTCCAGGTGTGCCCATGTGGGGCAAACGTGACCCTGAGCTGCCAGTCTCCAAGG
DNA35639	660	AGTAAGCCGCTGTCCAATACCAAGTGGGATCGCAGCTCCATCCTCCAGACTTTCTT *****
P_AAF45014	687	AGTAAGCCGCTGTCCAATACCAAGTGGGATCGCAGCTCCATCCTCCAGACTTTCTT
DNA35639	720	GCACCAGCATTAGATGTCATCCGTGGTCTTAAGCCTCACCAACCTTCGTCTTCCATG *****
P_AAF45014	747	GCACCAGCATTAGATGTCATCCGTGGTCTTAAGCCTCACCAACCTTCGTCTTCCATG
DNA35639	780	GCTGGAGTCTATGTCATGCCAGGCCCCACAATGAGGTGGGACTGCCAATGTAATGTGACG *****
P_AAF45014	807	GCTGGAGTCTATGTCATGCCAGGCCCCACAATGAGGTGGGACTGCCAATGTAATGTGACG
DNA35639	840	CTGGAAGTGAGCACAGGCCCTGGAGCTGCAGTGGTGCTGGAGCTGTTGGGTACCCCTG *****
P_AAF45014	867	CTGGAAGTGAGCACAGGCCCTGGAGCTGCAGTGGTGCTGAAGCTGTTGGGTACCCCTG
DNA35639	900	GTTGGACTGGGTTGCTGGCTGGCTGGCCTTGTACCAACCGCGGGCAAGGCCCTG *****
P_AAF45014	927	GTTGGACTGGGTTGCTGGCTGGCTGGCCTTGTACCAACCGCGGGCAAGGCCCTG
DNA35639	960	GAGGAGCCAGCCAATGATATCAAGGAGGATGCCATTGCTCCCCGACCTGCCCTGGCCC *****
P_AAF45014	987	GAGGAGCCAGCCAATGATATCAAGGAGGATGCCATTGCTCCCCGACCTGCCCTGGCCC
DNA35639	1020	AAGAGCTCAGACACAATCTCCAAGAATGGGACCCCTTCCTCTGTCACCTCCGACGAGCC *****
P_AAF45014	1047	AAGAGCTCAGACACAATCTCCAAGAATGGGACCCCTTCCTCTGTCACCTCCGACGAGCC
DNA35639	1080	CTCCGGCCACCCCATGGCCCTCCAGGCCTGGTGCATTGACCCCCACGCCAGTCTCTCC *****
P_AAF45014	1107	CTCCGGCCACCCCATGGCCCTCCAGGCCTGGTGCATTGACCCCCACGCCAGTCTATCC
DNA35639	1140	AGCCAGGCCCTGCCCTACCAAGAC-TGCCACGACAGATGGGGCCACCCCTCAACCAAT *****
P_AAF45014	1167	AGCCAGGCCCTGCCCTACCAAGACATGCCACGACAGATGGGGCCACCCCTCAACCAAT

Blast results A-39

DNA35639	1199	ATCCCCCATCCCTGGTGGGTTCTCCTCTGGC-TTGAGCCGCATGGTGCTGTGCCTG *****
P_AAF45014	1227	ATCCCCCATCCCTGGTGGGTTCTCCTCTGGC-TTGAGCCGCATGGTGCTGTGCCTG
DNA35639	1258	TGATGGTGCCTGCCAGAGTCAGCTGGCTCTGGTATGACCCCACCACTCATTGG *****
P_AAF45014	1287	TGATGGNGCCTGCCAGAGTCAGCTGGCTCTGGTATGACCCCACCACTCATTGG
DNA35639	1318	CTAAAGGATTGGGGTCTCTCCTATAAGGTACACCTCTAGCACAGAGGCCTGAGTC *****
P_AAF45014	1347	CTAAAGGATTGGGGTCTCTCCTATAAGGTACACCTCTAGCACAGAGGCCTGAGTC
DNA35639	1378	ATGGGAAAGAGTCACACTCCTGACCCTAGTACTCTGCCACCTCTTTACTGTGGG *****
P_AAF45014	1407	ATGGGAAAGAGTCACACTCCTGACCCTAGTACTCTGCCACCTCTTTACTGTGGG
DNA35639	1438	AAAACCATCTCAGTAAGACCTAACGTGTCCAGGAGACAGAAGGAGAAGAGGAAGTGGATCT *****
P_AAF45014	1467	AAAACCATCTCAGTAAGACCTAACGTGTCCAGGAGACAGAAGGAGAAGAGGAAGTGGATCT
DNA35639	1498	GGAATTGGGAGGAGCCTCACCCACCCCTGACTCCTCTTATGAAGCCAGCTGCTGAAAT *****
P_AAF45014	1527	GGAATTGGGAGGAGCCTCACCCACCCCTGACTCCTCTTATGAAGCCAGCTGCTGAAAT
DNA35639	1558	TAGCTACTCACCAAGAGTGAGGGCAGAGACTTCCAGTCAGTCACTGAGTCTCCAGGCCCCCT *****
P_AAF45014	1587	TAGCTACTCACCAAGAGTGAGGGCAGAGACTTCCAGTCAGTCACTGAGTCTCCAGGCCCCCT
DNA35639	1618	TGATCTGTACCCACCCCTATCTAACACCACCTGGCTCCACTCCAGCTCCGTATT *****
P_AAF45014	1647	TGATCTGTACCCACCCCTATCTAACACCACCTGGCTCCACTCCAGCTCCGTATT
DNA35639	1678	GATATAACCTGTCAGGCTGGCTGGTTAGGTTTACTGGGCAGAGGATAGGAATCTCT *****
P_AAF45014	1707	GATATAACCTGTCAGGCTGGCTGGTTAGGTTTACTGGGCAGAGGATAGGAATCTCT
DNA35639	1738	TATTAAGAACTAACATGAAATATGTGTTTTCAATTGCAAATTAAATAAGATACATA *****
P_AAF45014	1767	TATTAAGAACTAACATGAAATATGTGTTTTCAATTGCAAATTAAATAAGATACATA
DNA35639	1798	ATGTTGTATGA *****
P_AAF45014	1827	ATGTTGTATGA